

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 17, 2006, 10:45:07 ; Search time 2012 Seconds
(without alignments)
6502.066 Million cell updates/sec

Title: US-10-649-193-14
Perfect score: 1582
Sequence: 1 CGAGCCGCGAGCGCGCGC.....gtctctccctgcagccgtg 1582

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA_Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	1582	100.0	1582	7	US-10-649-193-14
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4	1398	88.4	1495	7	US-10-649-193-1
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6	1396.4	88.3	2536	3	US-09-799-978-1
7	1396.4	88.3	2536	7	US-10-649-852-1
8	1335	84.4	1335	6	US-10-305-720-1360
9	1188	75.1	1285	3	US-09-799-978-3
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45	600	37.9	600	10	US-11-060-756-2448

ALIGNMENTS

RESULT 1
US-09-191-724-14
; Sequence 14, Application US/09191724
; Patent No. US20020055617A1
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: CRF Receptor(s)
; FILE REFERENCE: Salk1748
; CURRENT APPLICATION NUMBER: US/09/191,724
; CURRENT FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: US 08/374,009
; EARLIER FILING DATE: 1995-01-17
; EARLIER APPLICATION NUMBER: US 08/353,537
; EARLIER FILING DATE: 1994-12-09
; EARLIER APPLICATION NUMBER: PCT/US94/05908
; EARLIER FILING DATE: 1993-05-25
; EARLIER APPLICATION NUMBER: US 08/110,286
; EARLIER FILING DATE: 1993-08-23
; EARLIER APPLICATION NUMBER: US 08/079,320
; EARLIER FILING DATE: 1993-06-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1582
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)...(1413)
; OTHER INFORMATION: CRF-R splice-variant insert fragment inserted
; OTHER INFORMATION: between nucleotides 516-517 of SEQ ID NO:1.
; OTHER INFORMATION: /note= "This sequence is contained in clone
; OTHER INFORMATION: "CRF-R2".
US-09-191-724-14

Query Match 100.0%; Score 1582; DB 3; Length 1582;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAGCCGCGAGCGCGCGCGTCTCTGGGATGTCCTAGGACCGCGGCATTAGGAC 60

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QY      61  GGTAGCGAGCGAGCGCGAGATGGAGGACCGCGAGCTCCGTCTCGTCAAGGCCCTT 120
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QY     181  TCCTGCGCCAGCAACATCTCAGGACTGCAAGTGCAGACGCAATCCGTGGACCTCATTTGGCACC 240
Db     181  TCCTGCGCCAGCAACATCTCAGGACTGCAAGTGCAGACGCAATCCGTGGACCTCATTTGGCACC 240
QY     241  TGTGCGCCCGCAGCGCTGCGGGGCGAGCTAGTGGTTGCGGCCCTGCGCTGCTTTTCTAT 300
Db     241  TGTGCGCCCGCAGCGCTGCGGGGCGAGCTAGTGGTTGCGGCCCTGCGCTGCTTTTCTAT 300
QY     301  GGTGTCCGCTACAAATACCAAAATGGCTACCGGAGTGCCTGGCCAAATGCGAGCTGG 360
Db     301  GGTGTCCGCTACAAATACCAAAATGGCTACCGGAGTGCCTGGCCAAATGCGAGCTGG 360
QY     361  GCGCCCGCGGTGAATTAATCCGAGTGCAGGAGATCCTCAATGAGGAGAAAAAGCAAG 420
Db     361  GCGCCCGCGGTGAATTAATCCGAGTGCAGGAGATCCTCAATGAGGAGAAAAAGCAAG 420
QY     421  GTGCACTACATGTCCGAGTCAATCAACTACTGCGGCGCACTGTATCTCCCTGGTGGCC 480
Db     421  GTGCACTACATGTCCGAGTCAATCAACTACTGCGGCGCACTGTATCTCCCTGGTGGCC 480
QY     481  CTCCTGTGGCTTTGTCCTCTTCTGCGCTCAGGCGAGGCTGCAACCTATGGGGTGAC 540
Db     481  CTCCTGTGGCTTTGTCCTCTTCTGCGCTCAGGCGAGGCTGCAACCTATGGGGTGAC 540
QY     541  CAGGCGAGATGGAGCCCTGGAGGTGGGGGCTCCATGGAGTGGTCCCACTTCAGGTTTGA 600
Db     541  CAGGCGAGATGGAGCCCTGGAGGTGGGGGCTCCATGGAGTGGTCCCACTTCAGGTTTGA 600
QY     601  AGAGAGCATCCGGTGCCTGCGAAACATCATCCACTGGAACCTCATCTCGGCTTCATCCTG 660
Db     601  AGAGAGCATCCGGTGCCTGCGAAACATCATCCACTGGAACCTCATCTCGGCTTCATCCTG 660
QY     661  CGCAAGCCACCTGTTGCTGTTGCTGCTCCAGTAAACATAGAGCCCGAGTCCACAGAGCAAC 720
Db     661  CGCAAGCCACCTGTTGCTGTTGCTGCTCCAGTAAACATAGAGCCCGAGTCCACAGAGCAAC 720
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Db     721  GTGGGCTGTGTGAGGTTGTGTGACAGCGCGCTCAACTACTTCCATGTGACCAACTTTCTTC 780
QY     781  TGGATGTTGGCGAGGCTGCTACTGTCACAGCCATCGTGTCTACCTACTCTCACTGAC 840
Db     781  TGGATGTTGGCGAGGCTGCTACTGTCACAGCCATCGTGTCTACCTACTCTCACTGAC 840
QY     841  CGGCTCGGCAAAATGGAATGTTCACTGATGGCTGGGGTGGCCCTCCCACTCATTTGTG 900
Db     841  CGGCTCGGCAAAATGGAATGTTCACTGATGGCTGGGGTGGCCCTCCCACTCATTTGTG 900
QY     901  GCCTGGGCCCATTTGGGAAGCTGTACTAGCAATGAGAAGTGCCTGTTTGGCAAAAGGCCCT 960
Db     901  GCCTGGGCCCATTTGGGAAGCTGTACTAGCAATGAGAAGTGCCTGTTTGGCAAAAGGCCCT 960
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Db     961  GGGGTGTACACCGATACATCTACAGGGGCCCATGATCTCGTCTGCTGTGATCAATTC 1020
QY    1021  ATCTTCTTTTCAACATGTCGCGCATCTCTACACCAAGCTCCGGGATCCACAGCTCT 1080
Db    1021  ATCTTCTTTTCAACATGTCGCGCATCTCTACACCAAGCTCCGGGATCCACAGCTCT 1080
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Db     1141  ATCACTTACATGCTGTTCTTCTGATCAATCCGGGGAGGATGAGGTCTCCCGGGTCTGTTTC 1200
QY     1201  ATCTACTTCAACTCCTTCTCGTAATCTTTCAGGGCTCTTTTGTGCTGTTGTTCTACTGT 1260
Db     1201  ATCTACTTCAACTCCTTCTCGTAATCTTTCAGGGCTCTTTTGTGCTGTTGTTCTACTGT 1260
QY     1261  TTCTCTCAATPAGTAGGTCCGTTCTTGCCATTCGGAAGAGGTGGCAACGGTGGCAGGACAAG 1320
Db     1261  TTCTCTCAATPAGTAGGTCCGTTCTTGCCATTCGGAAGAGGTGGCAACGGTGGCAGGACAAG 1320
QY     1321  CACTCGATCCGTCGCGAGTGGCCGCTGTCATGTCATCCCACTCCCAACCCGTTCT 1380
Db     1321  CACTCGATCCGTCGCGAGTGGCCGCTGTCATGTCATCCCACTCCCAACCCGTTCT 1380
QY     1381  AGCTTTTACAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCTATGGAGAGCCCC 1440
Db     1381  AGCTTTTACAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCTATGGAGAGCCCC 1440
QY     1441  CAAAGAGCTGTGGCTGGGGGATGACGGCCAGGCTCCCTGACCACTGCTGTGGAGGT 1500
Db     1441  CAAAGAGCTGTGGCTGGGGGATGACGGCCAGGCTCCCTGACCACTGCTGTGGAGGT 1500
QY     1501  GACCTGTTAGGTCTCATGTCCTCCCACTCCCAAGAGCAGTGGCACTGACAGCTGGGGGG 1560
Db     1501  GACCTGTTAGGTCTCATGTCCTCCCACTCCCAAGAGCAGTGGCACTGACAGCTGGGGGG 1560
QY     1561  CGCTCTCTCCCTGACAGCCGTG 1582
Db     1561  CGCTCTCTCCCTGACAGCCGTG 1582
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RESULT 2

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US-10-649-193-14
; Sequence 14, Application US/10649193
; Publication No. US20040039173A1
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: CRF Receptor(s)
; FILE REFERENCE: Salk1748
; CURRENT APPLICATION NUMBER: US/10/649,193
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/191,724
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/374,009
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/353,537
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-12-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US94/05908
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-05-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/110,286
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-08-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/079,320
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-06-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1582
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)...(1413)
; OTHER INFORMATION: CRF-R splice-variant insert fragment inserted
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/ SEQ ID NO 1
/ LENGTH: 1495
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (82)...(1326)
/ OTHER INFORMATION: /product = "Human pituitary CRF-receptor"
/ OTHER INFORMATION: /note= "This sequence is encoded by clone
/ OTHER INFORMATION: "CRF-R1".
US-09-191-724-1

Query Match      88.4%; Score 1398; DB 3; Length 1495;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 1 CGAGCCGCGAGCCGCGCGCGTCTCTGGGATGTCCTAGGACCCGGGCAATTCAGGAC 60
DB 1 CGAGCCGCGAGCCGCGCGCGTCTCTGGGATGTCCTAGGACCCGGGCAATTCAGGAC 60

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DB 61 GGTAGCCGAGCGAGCCGCGAGGATGGAGGCGACCCCGCAGCTCCGTCCTCAAGGCCCTT 120

QY 121 CTCCTTCTGGGGGTGAACCCCGTCTCTGCTCCCTCCAGGACCGAGCACTGCGAGAGCCTG 180
DB 121 CTCCTTCTGGGGGTGAACCCCGTCTCTGCTCCCTCCAGGACCGAGCACTGCGAGAGCCTG 180

QY 181 TCCTGCGCAGCAATCTCAGACTGCAAGTGCATCGCAACGCAATCGTGAGCTCTATTTGGAC 240
DB 181 TCCTGCGCAGCAATCTCAGACTGCAAGTGCATCGCAACGCAATCGTGAGCTCTATTTGGAC 240

QY 241 TGTGCGCCCGAGCCCTGCGGGGCGAGTAGTGGTTCGGCCCTGCTGCTGCTTTTCTAT 300
DB 241 TGTGCGCCCGAGCCCTGCGGGGCGAGTAGTGGTTCGGCCCTGCTGCTGCTTTTCTAT 300

QY 301 GGTGTCCGCTACAAATACCAAAACAAATGGCTACCGGGAGTGCCTTGGCCAAATGGCAGCTG 360
DB 301 GGTGTCCGCTACAAATACCAAAACAAATGGCTACCGGGAGTGCCTTGGCCAAATGGCAGCTG 360

QY 361 GCGCCGCGGTGAATTTACTCCGAGTGCGCAGGAGATCTCAATGAGGAGAAAAAAGCAAG 420
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QY 481 CTCCTGTGGCCCTTTGTCTCTTTCTGCGGCTCAGGCCAGGCTGCACCCATTTGGGGTGAC 540
DB 481 CTCCTGTGGCCCTTTGTCTCTTTCTGCGGCTC----- 513

QY 541 CAGGCGAGTGGAGCCCTCGGAGGTGGGGGCTCCATGGAGTGGTCCCCCATTTTCAGTTGGA 600
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QY 601 AGGAGCATCGGTGCGTGGAAACATCATCCACTGGAACTCATCTCCGCTTCATCCTTG 660
DB 514 AGGAGCATCGGTGCGTGGAAACATCATCCACTGGAACTCATCTCCGCTTCATCCTTG 573

QY 661 CGCAAGCCCACTGGTGTGGTCCAGTCAACCATGAGCCCGAGGTCCACCAAGAGCAAC 720
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RESULT 4

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US-10-649-193-1
; Sequence 1, Application US/10649193
; Publication No. US20040039173A1
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; FILE REFERENCE: Salk1748
; CURRENT FILING DATE: 2003-08-26
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-12
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-01-17
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: US 08/374,009
; PRIOR APPLICATION NUMBER: US 08/353,537
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Qy	961	GGGGTGTACACGACATACATCTTACCAAGGGCCCATGATCTCTGGTCTCTGTGATCAATTTC	1020
Db	1547	GGGGTGTACACGACATACATCTTACCAAGGGCCCATGATCTCTGGTCTCTGTGATCAATTTC	1488
Qy	1021	ATCTTCTCTTTTCAACATCGTCCGCATCTCATGACCAAGCTCCGGGGCATCCACACGTCT	1080
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Qy	1081	GAGACCAATTCAGTACAGGAAGCGTGTGAAGCCACTCTGTGTCTGTGCCCCCTCTCTGGGC	1140
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Qy	1141	ATCACCTACATGCTGTTTCTTCTGTCATATCCCGGGAGGATGAGGTCTCCCGGTCTCTTTC	1200
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Qy	1261	TTCTCTCAATAGTGAAGTCCGTTCTGCCATCCGGAAGAGTGGACCGGTGGCAGGACAAG	1320
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Qy	1381	AGCTTTTCACAGCATCAAGCAGTCCACGACAGTCTGAGCTGGCAGGTCAATGGACGACGCC	1440
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Qy	1441	CAAGAGCTGTGGCTGGGGGATGACGGCCAGGCTCCCTGACCAACCTGCTGTGGAGGT	1500
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Db	947	CCGCTCTCCCGCTGCAGCCGTG 926	

RESULT 6

US-09-799-978-1

Sequence 1, Application US/09799978

Publication No. US20030165807A1

GENERAL INFORMATION:

APPLICANT: The Procter & Gamble Company

APPLICANT: Isfort, Robert

APPLICANT: Sheldon, Russell

TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscles

TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors

FILE REFERENCE: 8448

CURRENT APPLICATION NUMBER: US/09/799,978

CURRENT FILING DATE: 2001-03-06

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patent in version 3.0

SEQ ID NO 1

LENGTH: 2536

Query Match 88.3%; Score 1396.4; DB 7; Length 2536;
Best Local Similarity 94.4%; Pred. No. 0;
Matches 1494; Conservative 0; Mismatches 1; Indels 87; Gaps 1;
QY 1 CGAGCCGCGAGCCGCGCGCGTCTCTGGAGTGTCCGTAGGACCCGGGCAATTCAGGAC 60
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QY 361 GCCCGCGGTGAATTAATCCGAGTGCAGAGATCTCAATGAGGAGAAAAAGCAAG 420
DB 506 GCCCGCGGTGAATTAATCCGAGTGCAGAGATCTCAATGAGGAGAAAAAGCAAG 565
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QY 541 CAGGCAAGTGGAGCCCTCGGAGTGGGGGCTCCATGAGTGGTCCCAATTCAGGTTGGA 600
DB 659 ----- 658
QY 601 AGGAGCATCCGCTCGGAAATCATCCATCTGGAACTCATCTCCGCTTCATCCCTG 660
DB 659 AGGAGCATCCGCTCGGAAATCATCCATCTGGAACTCATCTCCGCTTCATCCCTG 718
QY 661 CGCAACGCCACCTGGTTCGTTCCAGCTAACATGAGCCCGAGGTCCACCAAGAGCAAC 720
DB 719 CGCAACGCCACCTGGTTCGTTCCAGCTAACATGAGCCCGAGGTCCACCAAGAGCAAC 778
QY 721 GTGGGCTGGTGCAGTGGTGAAGCGGCTTAACTTCTCATGTGACCAATCTTCT 780
DB 779 GTGGGCTGGTGCAGTGGTGAAGCGGCTTAACTTCTCATGTGACCAATCTTCT 838
QY 781 TGGATCTTCGGCAGGCTGTACCTGCAACAGCCATCGTGTCACTTCTCACTGAC 840
DB 839 TGGATCTTCGGCAGGCTGTACCTGCAACAGCCATCGTGTCACTTCTCACTGAC 898
QY 841 CGGCTCGCAAAATGGATGTTTCATCTGATTTGGCTGGGGTGTGCCCTTCCCATCATTTG 900
DB 899 CGGCTCGCAAAATGGATGTTTCATCTGATTTGGCTGGGGTGTGCCCTTCCCATCATTTG 958
QY 901 GCTTGGGCCAATGGAGCTGTACTAGCAATGAGAGTGTGGTTGGCAAAAGGCTT 960
DB 959 GCTTGGGCCAATGGAGCTGTACTAGCAATGAGAGTGTGGTTGGCAAAAGGCTT 1018
QY 961 GGGGTGTACACCACTACATCTACCGGGGCCCATGATCTCTGTCTGTGATCAATTT 1020
DB 1019 GGGGTGTACACCACTACATCTACCGGGGCCCATGATCTCTGTCTGTGATCAATTT 1078
QY 1021 ATCTTCTCTTCAACATCGTCCGATCTCATGACCAAGCTCCGGGCAATCCACCACTCT 1080

DB 1079 ATCTTCTCTTCAACATCGTCCGATCTCATGACCAAGTCCGGGCAATCCACCACTCT 1138
QY 1081 GAGACCATTCAGTACAGGAAGGCTGTGAAAGCCACTCTGGTGTCTGCCCCCTCTCTGGGC 1140
DB 1139 GAGACCATTCAGTACAGGAAGGCTGTGAAAGCCACTCTGGTGTCTGCCCCCTCTCTGGGC 1198
QY 1141 ATCACCCTACATGCTGTCTTCTGTCATCCCGGGAGGATGAGGTCTCCCGGGTCTCTTC 1200
DB 1199 ATCACCCTACATGCTGTCTTCTGTCATCCCGGGAGGATGAGGTCTCCCGGGTCTCTTC 1258
QY 1201 ATCTACTTCAACTCTCTTCTGGAATCTTCCAGGGCTTCTTGTGTCTGTGTCTACTGT 1260
DB 1259 ATCTACTTCAACTCTCTTCTGGAATCTTCCAGGGCTTCTTGTGTCTGTGTCTACTGT 1318
QY 1261 TTCTCTCAATAGTAGGTCTCGTCTTCTGCAATCCGGAAGAGGTGGCACCGGTGGCAAGCAAG 1320
DB 1319 TTCTCTCAATAGTAGGTCTCGTCTTCTGCAATCCGGAAGAGGTGGCACCGGTGGCAAGCAAG 1378
QY 1321 CACTCGATCCGTCGCGAGTGGCCGTGTCATGTCATCCCACTCCCACTCCCACTCCCACTCC 1380
DB 1379 CACTCGATCCGTCGCGAGTGGCCGTGTCATGTCATCCCACTCCCACTCCCACTCCCACTCC 1438
QY 1381 AGCTTTTCAAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCTATGGAGCAGCCCC 1440
DB 1439 AGCTTTTCAAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCTATGGAGCAGCCCC 1498
QY 1441 CAAAGAGCTGTGGCTGGGGGATGACGGCCAGGCTCCCTGACCACTGCTGTGGAGGT 1500
DB 1499 CAAAGAGCTGTGGCTGGGGGATGACGGCCAGGCTCCCTGACCACTGCTGTGGAGGT 1558
QY 1501 GACCTGTAGGTCTCATGCCCCTCCCAAGGAGCAGTGGCACTGACAGCCTGGGGGGG 1560
DB 1559 GACCTGTAGGTCTCATGCCCCTCCCAAGGAGCAGTGGCACTGACAGCCTGGGGGGG 1618
QY 1561 CGGCTCTCCCTTGCAGCCGTG 1582
DB 1619 CGGCTCTCCCTTGCAGCCGTG 1640
RESULT 8
US-10-305-720-1360
; Sequence 1360, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1360
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g408691
US-10-305-720-1360
Query Match 84.4%; Score 1335; DB 6; Length 1335;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 82 ATGGGAGGGGACCCGCGAGTCCGTCTCGTCAAGGGCCCTTCTCTCTGGGGCTGAACCCC 141
DB 1 ATGGGAGGGGACCCGCGAGTCCGTCTCGTCAAGGGCCCTTCTCTCTGGGGCTGAACCCC 60
QY 142 GTCTCTGCTCCCTCCAGGACCAAGCACTGCGAGAGCTCTCCTGCGCCAGCAACTCTCA 201

Db 694 CACCTACTCACTGACCGGCTGGCAAAATGATGTTTCACTGCTGATTTGGCTGGGGTGTGCC 753
Qy 885 CTTTCCCATCATTTGTGGCCCTGGGCCAATTTGGGAAGCTGTACTACGACAATGAGAAGTGTG 944
Db 754 CTTTCCCATCATTTGTGGCCCTGGGCCAATTTGGGAAGCTGTACTACGACAATGAGAAGTGTG 813
Qy 945 GTTTGGCAAAAGCCCTGGGGGTGTACACCGACTACATCTACAGGGCCCAATGATCCTGGT 1004
Db 814 GTTTGGCAAAAGCCCTGGGGGTGTACACCGACTACATCTACAGGGCCCAATGATCCTGGT 873
Qy 1005 CTTGCTGATCAATTTTCACTTCTTTTCAACATCGTCCGCACTCTCATGACCAAGCTCCG 1064
Db 874 CTTGCTGATCAATTTTCACTTCTTTTCAACATCGTCCGCACTCTCATGACCAAGCTCCG 933
Qy 1065 GGCATCCACACGCTGTAGACCAATTCATGTAAGGAAGCTGTGAAGCCCACTCTGTGTGT 1124
Db 934 GGCATCCACACGCTGTAGACCAATTCATGTAAGGAAGCTGTGAAGCCCACTCTGTGTGT 993
Qy 1125 GCTGCCCTCTTGGGATCACTTACATGCTGTTTCTTCTGTCATCCCGGGGAGGATGAGGT 1184
Db 994 GCTGCCCTCTTGGGATCACTTACATGCTGTTTCTTCTGTCATCCCGGGGAGGATGAGGT 1053
Qy 1185 CTCCTGGGCTGCTTCTTCACTTCACTTCACTTCTTCTGGAATCTTCCAGGGCTTCTTTGT 1244
Db 1054 CTCCTGGGCTGCTTCTTCACTTCACTTCTTCTGGAATCTTCCAGGGCTTCTTTGT 1113
Qy 1245 GTCTGTGTTCTACTGTTTCTCAATAGTAGGTCCGTTCTGCCATCCGGAAGAGGTGGCA 1304
Db 1114 GTCTGTGTTCTACTGTTTCTCAATAGTAGGTCCGTTCTGCCATCCGGAAGAGGTGGCA 1173
Qy 1305 CCGGTGGCAGGACAGCACTCGATCCGTGCCGAGTGCCCGTGCATGTCATCCCCAC 1364
Db 1174 CCGGTGGCAGGACAGCACTCGATCCGTGCCGAGTGCCCGTGCATGTCATCCCCAC 1233
Qy 1365 CTCCTCAACCCGTGCTAGCTTTTCAACAGCAATCAAGCACTCCACAGCACTCTGA 1416
Db 1234 CTCCTCAACCCGTGCTAGCTTTTCAACAGCAATCAAGCACTCCACAGCACTCTGA 1285

RESULT 11
US-10-450-097-30
; Sequence 30, Application US/10450097
; Publication No. US20040110252A1
; GENERAL INFORMATION:
; APPLICANT: Septegen Ltd
; TITLE OF INVENTION: Yeast-Based Assay
; FILE REFERENCE: DE/p701948PCT
; CURRENT APPLICATION NUMBER: US/10/450,097
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: GB 0030038.4
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 10042
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PREPXi-CRHR

US-10-450-097-30
Query Match 73.0%; Score 1154.2; DB 7; Length 10042;
Best Local Similarity 93.3%; Pred. No. 5.4e-310;
Matches 1253; Conservative 0; Mismatches 3; Indels 87; Gaps 1;
Qy 75 CCGGAGATGGGAGGGACCGCGAGCTCGTCTGTCAGAGCCCTTCTCTTGGGGCT 134
Db 1227 CTCTAGAAATGGGAGGGACCGCGAGCTCCGTCTGTCAGAGCCCTTCTCTTGGGGCT 1286
Qy 135 GAACCCCGTCTGCGCTCCCTCCAGGACAGCACTGCGAGAGCTGTCCTCGGCACAA 194
Db 1287 GAACCCCGTCTGCGCTCCCTCCAGGACAGCACTGCGAGAGCTGTCCTCGGCACAA 1346

Qy 195 CATCTCAGGACTGCACTGCAACGCACTCGTGGACCTCATTTGGCACCTGCTGGGCCCGCAG 254
Db 1347 CATCTCAGGACTGCACTGCAACGCACTCGTGGACCTCATTTGGCACCTGCTGGGCCCGCAG 1406
Qy 255 CCGTGGGGGAGCTAGTGTTCGGCCCTGCGCTCTTTTCTATGTTGCTCGCTACAA 314
Db 1407 CCGTGGGGGAGCTAGTGTTCGGCCCTGCGCTCTTTTCTATGTTGCTCGCTACAA 1466
Qy 315 TACCAAAACAATGGCTACCGGAGTCTTGGCAATGGCAGTGGGCGCCCGCGTGA 374
Db 1467 TACCAAAACAATGGCTACCGGAGTCTTGGCAATGGCAGTGGGCGCCCGCGTGA 1526
Qy 375 TTACTCCGAGTCCAGGAGATCTCAATGAGGAGAAAAAAGCAAGGTGCACTACCATGT 434
Db 1527 TTACTCCGAGTCCAGGAGATCTCAATGAGGAGAAAAAAGCAAGGTGCACTACCATGT 1586
Qy 435 CGCAGTCACTCAATCACTTACCTGGGCCACTGTATCTCCCTGGTGGCCCTCTGTGGCCTT 494
Db 1587 CGCAGTCACTCAATCACTTACCTGGGCCACTGTATCTCCCTGGTGGCCCTCTGTGGCCTT 1646
Qy 495 TGTCTCTTTTGTGGGCTCAGGCCAGGCTGCAACCAATTTGGGGTGACACGAGCAATGGAGC 554
Db 1647 TGTCTCTTTTGTGGGCTC----- 1665
Qy 555 CTTGGAGGTGGGGCTCCATGGAGTGTGCCCCCATTTTCAGTTTCGAGGAGGACATCCGGTG 614
Db 1666 -----AGGAGCATCCGGT 1679
Qy 615 CTTGCCAAAACATCATCACTGAACTCTATCCGGCTTTCATCTGCGCAACGCCACCTG 674
Db 1680 CTTGCCAAAACATCATCACTGAACTCTATCTCCGGCTTTCATCTGCGCAACGCCACCTG 1739
Qy 675 GTTCTGTGCTCAAGCTAAACCATGAGCCCGAGGTTCACAGAGCAACGTGGGCTGGTGCG 734
Db 1740 GTTCTGTGCTCAAGCTAAACCATGAGCCCGAGGTTCACAGAGCAACGTGGGCTGGTGCG 1799
Qy 735 GTTGTGACAGCGCCCTACAACTTCTTCCATGTGACCACTTCTTGTGATGTTCCGCGA 794
Db 1800 GTTGTGACAGCGCCCTACAACTTCTTCCATGTGACCACTTCTTGTGATGTTCCGCGA 1859
Qy 795 GGGCTGCTACTGCACACAGCCATCGTGTCTCACTTCCACTGACCGGCTGGCGCAATG 854
Db 1860 GGGCTGCTACTGCACACAGCCATCGTGTCTCACTTCCACTGACCGGCTGGCGCAATG 1919
Qy 855 GATGTTTCATCTGCAATTTGGTGGGCTGTGCGCTTCCCATCATTTGGGCTGGGCCATTTG 914
Db 1920 GATGTTTCATCTGCAATTTGGTGGGCTGTGCGCTTCCCATCATTTGGGCTGGGCCATTTG 1979
Qy 915 GAAGCTGTACTACGACAATGAGAGTGTGCTGTTTGGCAAAAGCCCTGGGCTGTACACCGA 974
Db 1980 GAAGCTGTACTACGACAATGAGAGTGTGCTGTTTGGCAAAAGCCCTGGGCTGTACACCGA 2039
Qy 975 CTACATCTACGAGGCGCCCATGATCTGCTGCTGATCAATTTTCATCTTCTTTTCAA 1034
Db 2040 CTACATCTACGAGGCGCCCATGATCTGCTGCTGATCAATTTTCATCTTCTTTTCAA 2099
Qy 1035 CATCGTCCGATCTCTCATGACCAAGTCCGGGATCCACACGTCTEAGACCAATTCAGTA 1094
Db 2100 CATCGTCCGATCTCTCATGACCAAGTCCGGGATCCACACGTCTEAGACCAATTCAGTA 2159
Qy 1095 CAGGAAGGCTGTGAAAGCCATCTGCTGCTGCTGCGCCCTCTGGGGATCACTTACATGCT 1154
Db 2160 CAGGAAGGCTGTGAAAGCCATCTGCTGCTGCTGCGCCCTCTGGGGATCACTTACATGCT 2219
Qy 1155 GTTCTTCTCAATCCCGGGAGGATGAGGTCTCCCGGGTCTTCTTCACTTCACTTCAACTC 1214
Db 2220 GTTCTTCTCAATCCCGGGAGGATGAGGTCTCCCGGGTCTTCTTCACTTCACTTCAACTC 2279
Qy 1215 CTTCTCTGGAATCTTCCAGGGCTTCTTTTGTGCTGTGTTCTACTGTTTCTCAATAGTGA 1274
Db 2280 CTTCTCTGGAATCTTCCAGGGCTTCTTTTGTGCTGTGTTCTACTGTTTCTCAATAGTGA 2339
Qy 1275 GGTCTGTTCTGCCATCCGGGAAGAGGTGGCACCGGTTGGCAGGACAGCACTCGATCCGTGC 1334

Db 2340 GGTCCGTTCTGCCATCCGGAAGAGTGGCACCGTGGCAGGACAAGCACTCGATCCGTGC 2399
Qy 1335 CCGAGTGGCCGCTGCGCATGTCATCCCACTCCCAACCCGCTGTCAGCTTTTCAGAGCAT 1394
Db 2400 CCGAGTGGCCGCTGCGCATGTCATCCCACTCCCAACCCGCTGTCAGCTTTTCAGAGCAT 2459
Qy 1395 CAAGCAGTCCACAGCAGCTCTGAG 1417
Db 2460 CAAGCAGTCCACAGCAGCTCTGAG 2482

RESULT 12
US-10-450-097-28
; Sequence 28, Application US/10450097
; Publication No. US20040110252A1
; GENERAL INFORMATION:
; APPLICANT: Septegen Ltd
; TITLE OF INVENTION: Yeast-Based Assay
; FILE REFERENCE: DE/p701948PCT
; CURRENT APPLICATION NUMBER: US/10/450,097
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: GB 0030038.4
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-097-28

Query Match 72.8%; Score 1151; DB 7; Length 1248;
Best Local Similarity 93.5%; Pred. No. 2.4e-309;
Matches 1248; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

Qy 82 ATGGGAGGGCACCAGCAGTCCGCTCTCGTCAAGGCCCTTCTCCTCTCTGGGGCTGAACCCC 141
Db 1 ATGGGAGGGCACCAGCAGTCCGCTCTCGTCAAGGCCCTTCTCCTCTCTGGGGCTGAACCCC 60
Qy 142 GTCTCTGCTCCCTCCAGGACACGACACTGCGAGAGCTGTCCTTGGCCAGCAACATCTCA 201
Db 61 GTCTCTGCTCCCTCCAGGACACGACACTGCGAGAGCTGTCCTTGGCCAGCAACATCTCA 120
Qy 202 GGAATGAGTGCACGATCCGCTGACCTCATTTGGACACCTGCTGGCCCGCAGCCCTGG 261
Db 121 GGAATGAGTGCACGATCCGCTGACCTCATTTGGACACCTGCTGGCCCGCAGCCCTGG 180
Qy 262 GGGCAGCTAGTGGTTCCGGCCCTGCGCTGCTTTTCTATGTTGTCGCTACAAATACACA 321
Db 181 GGGCAGCTAGTGGTTCCGGCCCTGCGCTGCTTTTCTATGTTGTCGCTACAAATACACA 240
Qy 322 AACAAATGGCTACCGGGAGTGCCTGGCCAAATGGCAGTGGCCCGCCCGCTGGAATTAATCC 381
Db 241 AACAAATGGCTACCGGGAGTGCCTGGCCAAATGGCAGTGGCCCGCCCGCTGGAATTAATCC 300
Qy 382 GAGTGCAGAGATCTCAATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 441
Db 301 GAGTGCAGAGATCTCAATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy 442 ATCATCAACTACCTGGGCACTGATCTCTGCTGGCCCTGCTGGTGGCCCTTTGTCCTC 501
Db 361 ATCATCAACTACCTGGGCACTGATCTCTGCTGGCCCTGCTGGTGGCCCTTTGTCCTC 420
Qy 502 TTTCTGCGGCTCAGGCCAGCGTGCACCCATTGGGGTGACGAGCAGATGGAGCCCTGGAG 561
Db 421 TTTCTGCGGCTC----- 432
Qy 562 GTGGGGGCTCCATGAGTGGTGGCCCAATTCAGGTTGAAAGGAGCATCCGGTGCCTGGCA 621
Db 433 -----AGGAGCATCCGGTGCCTGGCA 453
Qy 622 AACATCATCCACTGGAACCTCATCTCGGCTTTCATCTCGGCAACGCCACCTGTTGCTG 681

Db 454 AACATCATCCACTGGAACCTCATCTCCGCTTTCATCTCCGCAACGCCACCTGGTTCGTG 513
Qy 682 GTCCAGCTAACCATGAGCCCCGAGGTCCACAGAGAGAAAGTGGGTGGTGGAGTGGTG 741
Db 514 GTCCAGCTAACCATGAGCCCCGAGGTCCACAGAGAGAAAGTGGGTGGTGGAGTGGTG 573
Qy 742 ACAGCGGCTTACAACTACTTCCATGTGACAACTTCTCTCTGATGTTCCGGCAGGCTGC 801
Db 574 ACAGCGGCTTACAACTACTTCCATGTGACAACTTCTCTCTGATGTTCCGGCAGGCTGC 633
Qy 802 TACTTGCAACAGCCATGCTCTACCTACTCCATGACCCGCTGCGCAAAATGGATGTTTC 861
Db 634 TACTTGCAACAGCCATGCTCTACCTACTCCATGACCCGCTGCGCAAAATGGATGTTTC 693
Qy 862 ATCTGCATTTGGCTGGGGTGGCCCTTCCCATCATTTGGCCCTGGCCCATTTGGGAGCTG 921
Db 694 ATCTGCATTTGGCTGGGGTGGCCCTTCCCATCATTTGGCCCTGGCCCATTTGGGAGCTG 753
Qy 922 TACTAGCAATGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 981
Db 754 TACTAGCAATGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 813
Qy 982 TACCAGGGCCCATGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1041
Db 814 TACCAGGGCCCATGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 873
Qy 1042 CGCATCTCTATGACCAAGCTCCGGGATCCACCACTGAGACCAATTCAGTACAGGAAG 1101
Db 874 CGCATCTCTATGACCAAGCTCCGGGATCCACCACTGAGACCAATTCAGTACAGGAAG 933
Qy 1102 GCTGTGAAGCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1161
Db 934 GCTGTGAAGCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 993
Qy 1162 GTCAATCCCGGGAGGATGAGGTCTCCCGGGTCTCTTCTCATCTCTCAACTCTTCTCTG 1221
Db 994 GTCAATCCCGGGAGGATGAGGTCTCCCGGGTCTCTTCTCATCTCTCAACTCTTCTCTG 1053
Qy 1222 GAATCTTCCAGGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1281
Db 1054 GAATCTTCCAGGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1113
Qy 1282 TCTGCCATCCGAGAGGTGGCACCGGTGGCAGGACAAGCACTCCGATCCGTCGCGAGTG 1341
Db 1114 TCTGCCATCCGAGAGGTGGCACCGGTGGCAGGACAAGCACTCCGATCCGTCGCGAGTG 1173
Qy 1342 GCCGTGCCATGTCCATCCCACTCCCAACCCGCTGTCAGCTTTTCCAGCATCAAGCAG 1401
Db 1174 GCCGTGCCATGTCCATCCCACTCCCAACCCGCTGTCAGCTTTTCCAGCATCAAGCAG 1233
Qy 1402 TCCACAGCAGTCTGA 1416
Db 1234 TCCACAGCAGTCTGA 1248

RESULT 13
US-09-826-509-482
; Sequence 482, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsema, Karin
; APPLICANT: Lin, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13

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; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 482
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-482

Query Match      72.7%; Score 1149.4; DB 3; Length 1248;
Best Local Similarity 93.4%; Pred. No. 6.7e-309;
Matches 1247; Conservative 0; Mismatches 1; Indels 87; Gaps 1;

QY 82 ATGGGAGGACCCCGAGCTCGCTCGTCAAGGCGCTTCTCTCTCTGGGCTGAACCCC 141
DB 1 ATGGGAGGACCCCGAGCTCGCTCGTCAAGGCGCTTCTCTCTCTGGGCTGAACCCC 60

QY 142 GTCTCTGCCCTCCCTCAGGACCAAGCTCGAGAGCTGTCCCTGGCCAGCAACATCTCA 201
DB 61 GTCTCTGCCCTCCCTCAGGACCAAGCTCGAGAGCTGTCCCTGGCCAGCAACATCTCA 120

QY 202 GGATGCACTGCAACGCACTCCGTGACCTCATTTGGCACTGTGCGCCCGCAGCCCTGCG 261
DB 121 GGATGCACTGCAACGCACTCCGTGACCTCATTTGGCACTGTGCGCCCGCAGCCCTGCG 180

QY 262 GGGCAGCTAGTGGTGGCCCTGCGCCCTGCTTTTCTATGTGTGCGTCAATACACACA 321
DB 181 GGGCAGCTAGTGGTGGCCCTGCGCCCTGCTTTTCTATGTGTGCGTCAATACACACA 240

QY 322 AACAAATGGCTACCGGAGTGCTGCGCAATGCGAGCTGCGCGCGCGCGTGAATTTACTCC 381
DB 241 AACAAATGGCTACCGGAGTGCTGCGCAATGCGAGCTGCGCGCGCGCGTGAATTTACTCC 300

QY 382 GAGTGCAGGAGATCCTCAATGAGGAGAAAAAAGCAAGTGCGACTACCATGTGCGAGTC 441
DB 301 GAGTGCAGGAGATCCTCAATGAGGAGAAAAAAGCAAGTGCGACTACCATGTGCGAGTC 360

QY 442 ATCATCAACTACTCGGGCACTGTATCTCCCTGCTGGTGGCCCTCTGTGGCTTTGCTCTC 501
DB 361 ATCATCAACTACTCGGGCACTGTATCTCCCTGCTGGTGGCCCTCTGTGGCTTTGCTCTC 420

QY 502 TTTCTGCGGCTCAGGCCAGCTGCACCCATTTGGGTGTACCGGAGTGGAGCCCTGGAG 561
DB 421 TTTCTGCGGCTC----- 432

QY 562 GTGGGGGCTCCATGGAGTGGTGGCCCAATTTACAGTTTCAAGGAGCATCCGGTGGCTCGGA 621
DB 433 -----AGGAGCATCCGGTGGCTCGGA 453

QY 622 AACATCACTCACTGAACTCATCTCCGCTTTTCCTGCGCAACGCCCACTGGTTGCTG 681
DB 454 AACATCACTCACTGAACTCATCTCCGCTTTTCCTGCGCAACGCCCACTGGTTGCTG 513

QY 682 GTCCAGCTAACCATGAGCCCGGAGTCCACAGAGCAACGTTGGCTGGTGGAGTGGTG 741
DB 514 GTCCAGCTAACCATGAGCCCGGAGTCCACAGAGCAACGTTGGCTGGTGGAGTGGTG 573

QY 742 ACAGCGCGCTACAACTACTTTCATGTGACCAACTTCTTCTGATGTTCCGCGAGGCTGC 801
DB 574 ACAGCGCGCTACAACTACTTTCATGTGACCAACTTCTTCTGATGTTCCGCGAGGCTGC 633

QY 802 TACCTGCACACAGCCATCGTCTCACTCACTCACTGACCGGCTGCGCAATGATGTTTC 861
DB 634 TACCTGCACACAGCCATCGTCTCACTCACTCACTGACCGGCTGCGCAATGATGTTTC 693

QY 862 ATCTGCAATTGGCTGGGCTGGCCCTTCCGCCATCATTTGGCTGGCCATTTGGGAAGCTG 921
DB 694 ATCTGCAATTGGCTGGGCTGGCCCTTCCGCCATCATTTGGCTGGCCATTTGGGAAGCTG 753

QY 922 TACTACGACAATGAGAGTGTGTTTGGCAAAAGGCGCTGAGGCTGACCGACTACATC 981
DB 754 TACTACGACAATGAGAGTGTGTTTGGCAAAAGGCGCTGAGGCTGACCGACTACATC 813

QY 982 TACCAGGGCCCATGATCTCGTCTGTGTGATCAATTTTCATCTCTCTTTTCAACATCGTC 1041

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OM nucleic - nucleic search, using sw model

Run on: March 17, 2006, 10:35:52 ; Search time 389 Seconds
(without alignments)
7229.055 Million cell updates/sec

Title: US-10-649-193-14
Perfect score: 1582
Sequence: 1 CGAGCCGAGCGCCGCCG.....GCTCTCCCTCGAGCGCTG 1582

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5 COMB.seq:
3: /cgn2_6/ptodata/1/ina/6A COMB.seq:
4: /cgn2_6/ptodata/1/ina/6B COMB.seq:
5: /cgn2_6/ptodata/1/ina/H COMB.seq:
6: /cgn2_6/ptodata/1/ina/PTUS COMB.seq:
7: /cgn2_6/ptodata/1/ina/PP COMB.seq:
8: /cgn2_6/ptodata/1/ina/RE COMB.seq:
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1582	100.0	1582	3	US-09-580-734-14
3	1582	100.0	1582	3	US-08-374-009-14
4	1582	100.0	1582	3	US-09-191-724-14
5	1398	88.4	1495	3	US-08-482-746-1
6	1398	88.4	1495	3	US-09-580-734-1
7	1398	88.4	1495	3	US-08-374-009-1
8	1398	88.4	1495	3	US-09-191-724-1
9	1396.4	88.3	2536	3	US-09-799-978-1
10	1335	84.4	1335	3	US-09-016-434-1360
11	1283	81.1	1380	2	US-08-110-286A-1
12	1188	75.1	1285	3	US-09-799-978-3
13	1149.4	72.7	1248	3	US-09-826-509-482
14	1057	66.8	1206	3	US-09-799-978-7
15	1035.2	65.4	1411	3	US-08-482-746-5
16	1035.2	65.4	1411	3	US-09-580-734-5
17	1035.2	65.4	1411	3	US-08-374-009-5
18	1035.2	65.4	1411	3	US-09-191-724-5
19	1035.2	65.4	1411	3	US-09-799-978-15
20	1013.4	64.1	1248	3	US-09-799-978-39
21	1006.8	63.6	2273	3	US-09-799-978-21
22	1003.8	63.5	1248	3	US-09-799-978-27
23	967	61.1	1248	2	US-08-110-286A-5
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27 622 39.3 1442 3 US-09-799-978-35 Sequence 35, Appl
28 617.8 39.1 1248 3 US-09-799-978-29 Sequence 29, Appl
29 559.6 35.4 1600 3 US-09-799-978-11 Sequence 11, Appl
30 557.8 35.3 1468 2 US-08-381-433A-7 Sequence 7, Appl
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32 557.8 35.3 2110 3 US-09-016-434-1070 Sequence 1070, Ap
33 557.8 35.3 2110 3 US-09-799-978-9 Sequence 9, Appl
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36 545 34.5 1626 3 US-09-799-978-17 Sequence 17, Appl
37 545 34.5 1626 2 US-09-881-401-3 Sequence 3, Appl
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41 541 34.2 1514 3 US-09-799-978-19 Sequence 19, Appl
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43 531 33.6 1374 3 US-09-580-734-9 Sequence 9, Appl
44 531 33.6 1374 3 US-08-374-009-9 Sequence 9, Appl
45 531 33.6 1374 3 US-09-191-724-9 Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-08-482-746-14
; Sequence 14, Application US/08482746B
; Patent No. 639315
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; FILE REFERENCE: P41-90002
; CURRENT APPLICATION NUMBER: US/08/482,746B
; CURRENT FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: US 08/374,009
; EARLIER FILING DATE: 1995-01-17
; EARLIER APPLICATION NUMBER: US 08/353,537
; EARLIER FILING DATE: 1994-12-09
; EARLIER APPLICATION NUMBER: PCT/US94/05908
; EARLIER FILING DATE: 1994-05-25
; EARLIER APPLICATION NUMBER: US 08/110,286
; EARLIER FILING DATE: 1993-08-23
; EARLIER APPLICATION NUMBER: US 08/079,320
; EARLIER FILING DATE: 1993-06-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1582
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)...(1413)
; OTHER INFORMATION: CRF-R splice-variant insert fragment inserted
; OTHER INFORMATION: between nucleotides 516-517 of SEQ ID NO:1.
; OTHER INFORMATION: /note= "This sequence is contained in clone
; OTHER INFORMATION: "CRF-R2".
US-08-482-746-14

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 541 CAGGAGATGGAGCCCTCGAGAGTGGGGGCTCCATGAGAGTGGTCCCATTTCAAGTTTGA 600
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Qy 661 CGCAACGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
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Db 781 TGGATGTTTGGCGAGGGCTGCTACCTGCACAGCCATCGTGTCACTACTCCACTGAC 840
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RESULT 2

US-09-580-734-14
; Sequence 14, Application US/09580734
; Patent No. 6482608
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; FILE REFERENCE: Salk1748
; CURRENT APPLICATION NUMBER: US/09/580,734
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/191,724
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/374,009
; PRIOR FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: US 08/353,537
; PRIOR FILING DATE: 1994-12-09
; PRIOR APPLICATION NUMBER: PCT/US94/05908
; PRIOR FILING DATE: 1993-05-25
; PRIOR APPLICATION NUMBER: US 08/110,286
; PRIOR FILING DATE: 1993-08-23
; PRIOR APPLICATION NUMBER: US 08/079,320
; PRIOR FILING DATE: 1993-06-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1582
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)...(1413)
; OTHER INFORMATION: CRP-R splice-variant insert fragment inserted
; OTHER INFORMATION: between nucleotides 516-517 of SEQ ID NO:1.

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RESULT 3
US-08-374-009-14
; Sequence 14, Application US/08374009A
; Patent No. 6495343
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: CRP Receptor(s)
; FILE REFERENCES: P41 9886
; CURRENT APPLICATION NUMBER: US/08/374,009A
; CURRENT FILING DATE: 1995-01-17
; EARLIER APPLICATION NUMBER: US 08/353,537
; EARLIER FILING DATE: 1994-12-09
; EARLIER APPLICATION NUMBER: US 08/079,320
; EARLIER FILING DATE: 1993-06-18
; EARLIER APPLICATION NUMBER: US 08/110,286
; EARLIER FILING DATE: 1993-08-23
; EARLIER APPLICATION NUMBER: PCT/US94/05908
; EARLIER FILING DATE: 1994-05-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1582
; TYPE: DNA

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/ CURRENT FILING DATE: 1995-06-07
/ EARLIER APPLICATION NUMBER: US 08/374,009
/ EARLIER FILING DATE: 1995-01-17
/ EARLIER APPLICATION NUMBER: US 08/353,537
/ EARLIER FILING DATE: 1994-12-09
/ EARLIER APPLICATION NUMBER: PCT/US94/05908
/ EARLIER FILING DATE: 1994-05-25
/ EARLIER APPLICATION NUMBER: US 08/110,286
/ EARLIER FILING DATE: 1993-08-23
/ EARLIER APPLICATION NUMBER: US 08/079,320
/ EARLIER FILING DATE: 1993-06-18
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 1495
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (82)...(1326)
/ OTHER INFORMATION: /product = "Human pituitary CRP-receptor"
/ OTHER INFORMATION: /note= "This sequence is encoded by clone
/ OTHER INFORMATION: "CRF-R1".
US-08-482-746-1

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Best Local Similarity 94.5%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

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RESULT 6
US-09-580-734-1
; Sequence 1, Application US/09580734
; Patent No. 6482608
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.

APPLICANT: Vale Jr., Wylie W.
APPLICANT: Donaldson, Cynthia J.
APPLICANT: Sawchenko, Paul
TITLE OF INVENTION: Cloning and Recombinant Production of
FILE REFERENCE: Salk1748
CURRENT APPLICATION NUMBER: US/09/580,734
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/191,724
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 08/374,009
PRIOR FILING DATE: 1995-01-17
PRIOR APPLICATION NUMBER: US 08/353,537
PRIOR FILING DATE: 1994-12-09
PRIOR APPLICATION NUMBER: PCT/US94/05908
PRIOR FILING DATE: 1993-05-25
PRIOR APPLICATION NUMBER: US 08/110,286
PRIOR FILING DATE: 1993-08-23
PRIOR APPLICATION NUMBER: US 08/079,320
PRIOR FILING DATE: 1993-06-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1495
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (82)...(1326)
OTHER INFORMATION: /product = "Human pituitary CRP-receptor"
OTHER INFORMATION: /note = "This sequence is encoded by clone
OTHER INFORMATION: "CRP-R1"."
US-09-580-734-1

Query Match 88.4%; Score 1398; DB 3; Length 1495;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;
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QY 1141 ATCACTGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
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QY 1201 ATCTACTTCAACTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
DB 1114 ATCTACTTCAACTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1173
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481	QY	CTCTGGTGGCCTTTTGTCTCTCTTTCTGCGGCTCAGGCCAGGCTGCACCCATTTGGGGTGAC	540
481	DB		513
541	QY	CTCTGGTGGCCTTTTGTCTCTTTCTGCGGCTC-----	600
514	DB	CAGGCAGATGAGACCCCTGGAGGTGGGGGCTCCATGAGGTGGTGCCTCCATTTCAGGTTGCA	600
601	QY	-----	513
514	DB	AGGAGCATCCGGTGCCTTCGGAACATCATTCGACTGGAACTCATCTCCGCTTCATCTCTG	560
514	DB	AGGAGCATCCGGTGCCTTCGGAACATCATTCGACTGGAACTCATCTCCGCTTCATCTCTG	573
661	QY	CGCAACCGCACCTGGTTCTGTGTTCAGCTTAACATGAGCCCCGAGGTCCACAGAGCAAC	720
574	DB	CGCAACCGCACCTGGTTCTGTGTTCAGCTTAACATGAGCCCCGAGGTCCACAGAGCAAC	633
721	QY	GTGGCTGGTGCAGGTTGGTGTGACAGCGCTACAACCTACTTCCATGTGTGACCAACTTCTTC	780
634	DB	GTGGCTGGTGCAGGTTGGTGTGACAGCGCTACAACCTACTTCCATGTGTGACCAACTTCTTC	693
781	QY	TGGATGTTGGCGAGGGCTGCTACTGTGACACAGCCATCGTGGTCACTTCTCCACTGTAC	840
694	DB	TGGATGTTGGCGAGGGCTGCTACTGTGACACAGCCATCGTGGTCACTTCTCCACTGTAC	753
841	QY	CGGCTGCGCAATGGATGTTCACTGTCAATTTGGCTGGGGTGTGCCCTTCCCCATCATTTGTG	900
754	DB	CGGCTGCGCAATGGATGTTCACTGTCAATTTGGCTGGGGTGTGCCCTTCCCCATCATTTGTG	813
901	QY	GCTTGGGCCATTGGGAAGCTGTACTACGACAATGAGAAGTGTGGTTTGGCAAAAGGCCT	960
814	DB	GCTTGGGCCATTGGGAAGCTGTACTACGACAATGAGAAGTGTGGTTTGGCAAAAGGCCT	873
961	QY	GGGGTGTAACCGACTACATCTACAGAGGCCCAATGATCTGGTCTGTGTGATCAATTTTC	1020
874	DB	GGGGTGTAACCGACTACATCTACAGAGGCCCAATGATCTGGTCTGTGTGATCAATTTTC	933
1021	QY	ATCTTCCTTTTCAACATCGTCCGATCTCATGACCAAGCTCGGGCATCCACAGTCT	1080
934	DB	ATCTTCCTTTTCAACATCGTCCGATCTCATGACCAAGCTCGGGCATCCACAGTCT	993
1081	QY	GAGACCAITTCAGTACAGGAAGGCTGTGAAAGCCACTCTGGTGTGTGTCGCCCTCTCTGGGC	1140
994	DB	GAGACCAITTCAGTACAGGAAGGCTGTGAAAGCCACTCTGGTGTGTGTCGCCCTCTCTGGGC	1053
1141	QY	ATCACCCTAATGCTGTTCTGTCATATCCCGGGAGGATGAGGTCTCCGGGTCTCTTC	1200
1054	DB	ATCACCCTAATGCTGTTCTGTCATATCCCGGGAGGATGAGGTCTCCGGGTCTCTTC	1113
1201	QY	ATCTACTTCAATCTCTTCCCTGGAATCCTTTCAGGGCTCTTTGTGTCTGTGTCTACTGT	1260
1114	DB	ATCTACTTCAATCTCTTCCCTGGAATCCTTTCAGGGCTCTTTGTGTCTGTGTCTACTGT	1173
1261	QY	TTCTCTCAATAGTGAGGTCCGTTCTGTCATCCCGGAAGAGGTGGCACCGGTGGCAGGACAAG	1320
1174	DB	TTCTCTCAATAGTGAGGTCCGTTCTGTCATCCCGGAAGAGGTGGCACCGGTGGCAGGACAAG	1233
1321	QY	CACTCGATCCGTGCCGAGTGGCCGTGTGCAATGTCCATCCCACTCCCAACCCGTGTCT	1380
1234	DB	CACTCGATCCGTGCCGAGTGGCCGTGTGCAATGTCCATCCCACTCCCAACCCGTGTCT	1293
1381	QY	AGCTTTTCAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCATGGAGCAGCCCC	1440
1294	DB	AGCTTTTCAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCATGGAGCAGCCCC	1353
1441	QY	CAAGAAGCTGTGGCTGGGGGATGAGCGGCAGGCTCCCTGACCAACCTCTGTGTGAGGT	1500
1354	DB	CAAGAAGCTGTGGCTGGGGGATGAGCGGCAGGCTCCCTGACCAACCTCTGTGTGAGGT	1413
1501	QY	GACCTGTTAGGTCTCATGTCCCACTTCCCCCAGAGCAGCTGGCACTGACACCTCTGGGGGG	1560
1414	DB	GACCTGTTAGGTCTCATGTCCCACTTCCCCCAGAGCAGCTGGCACTGACACCTCTGGGGGG	1473

QY 1561 CCGCTCTCCCGCTGCGAGCCGTG 1582
Db 1474 CCGCTCTCCCGCTGCGAGCCGTG 1495

RESULT 8

US-09-191-724-1
; Sequence 1, Application US/09191724
; Patent No. 6638905
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; FILE REFERENCE: Salk1748
; CURRENT APPLICATION NUMBER: US/09/191,724
; CURRENT FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: US 08/374,009
; EARLIER FILING DATE: 1995-01-17
; EARLIER APPLICATION NUMBER: US 08/353,537
; EARLIER FILING DATE: 1994-12-09
; EARLIER APPLICATION NUMBER: PCT/US94/05908
; EARLIER FILING DATE: 1993-05-25
; EARLIER APPLICATION NUMBER: US 08/110,286
; EARLIER FILING DATE: 1993-08-23
; EARLIER APPLICATION NUMBER: US 08/079,320
; EARLIER FILING DATE: 1993-06-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1495
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)...(1326)
; OTHER INFORMATION: /product = "Human pituitary CRF-receptor"
; OTHER INFORMATION: /note = "This sequence is encoded by clone
; OTHER INFORMATION: "CRF-R1".
US-09-191-724-1

Query Match 88.4%; Score 1398; DB 3; Length 1495;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;
QY 1 CGAGCCCGCAGCCGCGCGGTCTCTGGGATGTCCTAGGACCCGGGCATTCAGGAC 60
Db 1 CGAGCCCGCAGCCGCGCGGTCTCTGGGATGTCCTAGGACCCGGGCATTCAGGAC 60
QY 61 GGTAGCCGAGCAGCCGCGAGGATGGAGGGACCCCGAGCTCCGTCTCGTCAAGGCCCTT 120
Db 61 GGTAGCCGAGCAGCCGCGAGGATGGAGGGACCCCGAGCTCCGTCTCGTCAAGGCCCTT 120
QY 121 CTCCTTCTGGGCTGACCCCGTCTGCTCCCTCCAGACCCAGCACTCGGAGGCGCTG 180
Db 121 CTCCTTCTGGGCTGACCCCGTCTGCTCCCTCCAGACCCAGCACTCGGAGGCGCTG 180
QY 181 TCCTGCGCAGCAACATCTCAGGACTGCAAGCATCCGTCGAGCTCATTTGGCACC 240
Db 181 TCCTGCGCAGCAACATCTCAGGACTGCAAGCATCCGTCGAGCTCATTTGGCACC 240
QY 241 TGCTGGCCCGCAGCCCTGCGGGGACGCTAGTGGTTTCGGCCCTGCCCTTTTCTAT 300
Db 241 TGCTGGCCCGCAGCCCTGCGGGGACGCTAGTGGTTTCGGCCCTGCCCTTTTCTAT 300
QY 301 GGTGTCCGCTACATACCAACAATGGCTACCGGAGTGCCTGGCCATGGCAGCTGG 360
Db 301 GGTGTCCGCTACATACCAACAATGGCTACCGGAGTGCCTGGCCATGGCAGCTGG 360

QY 361 GCGCCCGCGTGAATTACTCCGAGTCCAGGAGATCTCAATGAGGAGAAAAAGCAAG 420
Db 361 GCGCCCGCGTGAATTACTCCGAGTCCAGGAGATCTCAATGAGGAGAAAAAGCAAG 420
QY 421 GTGCACTACCATGTGCGAGTCACTCAACTACTTGGGCCACTGTATCTCCCTGGTGGCC 480
Db 421 GTGCACTACCATGTGCGAGTCACTCAACTACTTGGGCCACTGTATCTCCCTGGTGGCC 480
QY 481 CTCCTGGTGGCCCTTCTCTTTTCTGGGCTCAGGCCAGGCTGCACCCCATTTGGGGTGAC 540
Db 481 CTCCTGGTGGCCCTTCTCTCTTTCTCTGGGCTC----- 513
QY 541 CAGGCAGATGGAGCCCTCGAGGTGGGGGCTCCATGAGTGGTGGCCCATTTACAGTTTGA 600
Db 514 ----- 513
QY 601 AGGAGCATCCGGTGCCTCGGAAACATCATCACTGGAACCTCATCTCCGCTTTCATCTG 660
Db 514 AGGAGCATCCGGTGCCTCGGAAACATCATCACTGGAACCTCATCTCCGCTTTCATCTG 573
QY 661 CGCAACGCCACCTGGTTCGTGTCAGTAAACATGAGCCCGAGGTCCACGAGCAAC 720
Db 574 CGCAACGCCACCTGGTTCGTGTCAGTAAACATGAGCCCGAGGTCCACGAGCAAC 633
QY 721 GTGGGCTGGTGCAGGTGGTGACAGCGGCTCAACTACTTCCATGTGACCAACTTCTTC 780
Db 634 GTGGGCTGGTGCAGGTGGTGACAGCGGCTCAACTACTTCCATGTGACCAACTTCTTC 693
QY 781 TGGATGTTCGGCGAGGCTGTACTGTCACAGCCATCGTGTCTCACTACTTCCACTGAC 840
Db 694 TGGATGTTCGGCGAGGCTGTACTGTCACAGCCATCGTGTCTCACTACTTCCACTGAC 753
QY 841 CCGCTCGCAAAATGATGTTTCATCTGCTGGTGGGCTGGCCCTTCCCATCATTTGTG 900
Db 754 CCGCTCGCAAAATGATGTTTCATCTGCTGGTGGGCTGGCCCTTCCCATCATTTGTG 813
QY 901 GCCTGGGCCATTTGGGAAGCTGTACTAGCAATGAGAAGTCTGGTTTGGCAAAAGSCCT 960
Db 814 GCCTGGGCCATTTGGGAAGCTGTACTAGCAATGAGAAGTCTGGTTTGGCAAAAGSCCT 873
QY 961 GGGGTGTACACGACTACATCTACAGGCGCCCATGATCTCTGTCTCTGTGATCAATTTTC 1020
Db 874 GGGGTGTACACGACTACATCTACAGGCGCCCATGATCTCTGTCTCTGTGATCAATTTTC 933
QY 1021 ATCTTCTTTTCAACATCTGTCGCCATCTCATGACCAAGCTCCGGGCGATCCACACGCT 1080
Db 934 ATCTTCTTTTCAACATCTGTCGCCATCTCATGACCAAGCTCCGGGCGATCCACACGCT 993
QY 1081 GAGACCATTCAGTACAGGAAGCTGTGAAAGCCACTCTCTGTGTGTGTGCTCCCTCTGGGC 1140
Db 994 GAGACCATTCAGTACAGGAAGCTGTGAAAGCCACTCTCTGTGTGTGTGCTCCCTCTGGGC 1053
QY 1141 ATCACTCTCATGTGTCTTCTGTCATCCCGGGAGGATGAGGTCTCCCGGGTGTCTTC 1200
Db 1054 ATCACTCTCATGTGTCTTCTGTCATCCCGGGAGGATGAGGTCTCCCGGGTGTCTTC 1113
QY 1201 ATCTACTTCAACTCTCTTCTGGAATCTTCCAGGGCTTCTTTGTGTGTGTCTACTGT 1260
Db 1114 ATCTACTTCAACTCTCTTCTGGAATCTTCCAGGGCTTCTTTGTGTGTGTCTACTGT 1173
QY 1261 TTCTCTCAATAGTAGGTTCGTTCTTGCCATCCGGAAGAGGTGGCAACCGGTGGCAGCAAG 1320
Db 1174 TTCTCTCAATAGTAGGTTCGTTCTTGCCATCCGGAAGAGGTGGCAGCCGTTGGCAGCAAG 1233
QY 1321 CACTCGATCCGTGCGCGAGTGGCCGTCATGTCATCCCGACCTCCCAACCCGTGTC 1380
Db 1234 CACTCGATCCGTGCGCGAGTGGCCGTCATGTCATCCCGACCTCCCAACCCGTGTC 1293
QY 1381 AGCTTTTACAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCTATGGAGCAGCCCC 1440
Db 1294 AGCTTTTACAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCTATGGAGCAGCCCC 1353


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Db 1619 CCGCTCTCCCCCGACCGGTG 1640
|||||
RESULT 10
US-09-016-434-1360
; Sequence 1360, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1360:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g408691
; US-09-016-434-1360

Query Match 84.4%; Score 1335; DB 3; Length 1335;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 ATGGGAGGGACCCGAGCTCCGTCCTCGTCAAGGCCCTTCTCTCTTCTGGGGCTGAACCCC 141
Db 1 ATGGGAGGGACCCGAGCTCCGTCCTCGTCAAGGCCCTTCTCTCTTCTGGGGCTGAACCCC 60
QY 142 GTCTCTGCTCCCTCCAGGACAGCACTGCGAGAGCCCTGTCCTTGGCCAGCAATCTCA 201
Db 61 GTCTCTGCTCCCTCCAGGACAGCACTGCGAGAGCCCTGTCCTTGGCCAGCAATCTCA 120
QY 202 GGACTGCACTGCAAGCACTCCGTCCTGACCTCATTTGGCACCTGCTGGCCCGCAGCCCTGG 261
Db 121 GGACTGCACTGCAAGCACTCCGTCCTGACCTCATTTGGCACCTGCTGGCCCGCAGCCCTGG 180
QY 262 GGCAGCTAGTGTTCGGCCCTGCGCTGCTTTTCTATGCTGCTCCGCTACAATACCACA 321
Db 181 GGCAGCTAGTGTTCGGCCCTGCGCTGCTTTTCTATGCTGCTCCGCTACAATACCACA 240
QY 322 AACATGGCTACCGGGAGTGCCTGGCCAAATGGCAGCTGGGCCCGCCCGGTGAATTACTCC 381
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Db 1321 TCCACAGCAGTCTGA 1335

RESULT 11

US-08-110-286A-1

/ Sequence 1, Application US/08110286A

/ Patent No. 5728545

/ GENERAL INFORMATION:

/ APPLICANT: Perrin, Marilyn H.

/ APPLICANT: Chen, Ruoping

/ APPLICANT: Lewis, Kathy A.

/ APPLICANT: Vale Jr., Wylie W.

/ APPLICANT: Donaldson, Cynthia J.

/ TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF

/ NUMBER OF SEQUENCES: 6

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

/ STREET: 444 South Flower Street, Suite 2000

/ CITY: Los Angeles

/ STATE: CA

/ COUNTRY: USA

/ ZIP: 90071

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: PatentIn Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/110,286A

/ FILING DATE:

/ CLASSIFICATION: 435

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 08/079,320

/ FILING DATE: 18-JUN-1993

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Reiter, Stephen E.

/ REGISTRATION NUMBER: 31,192

/ REFERENCE/DOCKET NUMBER: P41 9439

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 619-546-4737

/ TELEFAX: 619-546-9392

/ INFORMATION FOR SEQ ID NO: 1:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 1380 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: both

/ TOPOLOGY: both

/ MOLECULE TYPE: cDNA

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: 82..1329 /product= "HUMAN PITUITARY

/ OTHER INFORMATION: CRF-RECEPTOR"

/ OTHER INFORMATION: /note= "This sequence is encoded by clone

/ OTHER INFORMATION: "CRF-R1".

US-08-110-286A-1

Query Match 81.1%; Score 1283; DB 2; Length 1380;

Best Local Similarity 94.1%; Pred. No. 4.8e-314;

Matches 1380; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 1 CGAGCCGAGCCGCGCGGTTCTCTGGGATGTCCTAGGACCGGGCATTGAGGAC 60

Db 1 CGAGCCGAGCCGCGCGGTTCTCTGGGATGTCCTAGGACCGGGCATTGAGGAC 60

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Db 61 GGTAGCGAGCGAGCGCGGATGGAGGACCGCGAGTCCGTCCTCGTCAAGGCCCTT 120

QY 121 CTCCTTCTGGGGCTGAACCCCGTCTCTGCTCCCTCCAGACCGAGACTGCGGAGGCTG 180

Db 121 CTCCTTCTGGGGCTGAACCCCGTCTCTGCTCCCTCCAGACCGAGACTGCGGAGGCTG 180

QY 181 TCCCTGGCCAGCAACATCTCAGGACTGCAAGCAACGCAATCCGTGGACCTCAATTGGCACC 240

Db 181 TCCCTGGCCAGCAACATCTCAGGACTGCAAGCAACGCAATCCGTGGACCTCAATTGGCACC 240

QY 241 TGTGTGCCCCCGAGCCCTGCGGGGAGCTAGTGTTCGGCCCTGCGCTCTTTTCTAT 300

Db 241 TGTGTGCCCCCGAGCCCTGCGGGGAGCTAGTGTTCGGCCCTGCGCTCTTTTCTAT 300

QY 301 GGTGTGCGCTACATACCAACAAATGCTACCGGAGTGCCTGGCCAAATGGCAGCTGG 360

Db 301 GGTGTGCGCTACATACCAACAAATGCTACCGGAGTGCCTGGCCAAATGGCAGCTGG 360

QY 361 GCGGCCGCGGTGAATTTACTCCAGTGCAGGAGATCTCAATGAGGAGAAAAAACAAG 420

Db 361 GCGGCCGCGGTGAATTTACTCCAGTGCAGGAGATCTCAATGAGGAGAAAAAACAAG 420

QY 421 GTGCACTACCATGTGCACTCATCATCACTACCTGGGCACTGTATCTCCCTGGTGGCC 480

Db 421 GTGCACTACCATGTGCACTCATCATCACTACCTGGGCACTGTATCTCCCTGGTGGCC 480

QY 481 CTCCTGGTGGCCCTTTGTCCTCTTTCTGGGGCTCAGGCCAGGCTGCACCATTTGGGGTGAC 540

Db 481 CTCCTGGTGGCCCTTTGTCCTCTTTCTGGGGCTC----- 513

QY 541 CAGGCAGATGGAGCCCTGAGGCTGGGGGCTCCATGAGGTGGTGCCTCAATTTCAGGTTTCCA 600

Db 541 ----- 513

QY 601 AGGAGCATCCGCTGCTGCGAAACATCATCTGGAACCTCATCTCCGCTTCATCTCTG 660

Db 601 AGGAGCATCCGCTGCTGCGAAACATCATCTGGAACCTCATCTCCGCTTCATCTCTG 660

QY 661 CGCAACGCCACCTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720

Db 661 CGCAACGCCACCTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720

QY 721 GTGGGCTGCTGCAAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

Db 721 GTGGGCTGCTGCAAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

QY 781 TGGATGTTCCGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840

Db 781 TGGATGTTCCGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840

QY 841 CGGCTGCGCAATGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900

Db 841 CGGCTGCGCAATGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900

QY 901 GCCTGGGCGCAATGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960

Db 901 GCCTGGGCGCAATGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960

QY 961 GGGGTGTACACCGACTACATCTACCGAGGCGCCCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020

Db 961 GGGGTGTACACCGACTACATCTACCGAGGCGCCCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020

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QY 1081 GAGACCATTCAGTACAGGAGGCTGTGAAAGGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140

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QY 1141 ATCACCCTACATGCTGTTCTTGTGCTCAATCCCGGGAGAGTGAAGTCTCCCGGGTCTGCTTTC 1200

Db 1141 ATCACCCTACATGCTGTTCTTGTGCTCAATCCCGGGAGAGTGAAGTCTCCCGGGTCTGCTTTC 1200

QY 1201 ATCTACTTCACTCTCTTCTGGAATCTTCCAGGGGCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1260

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QY 1261 TTCTCCTCAATAGTGGAGTCCGTTCTGCCATCCGGAAGAGGTGGCACCGGTGGCAGGACAAG 1320
DB 1174 TTCTCCTCAATAGTGGAGTCCGTTCTGCCATCCGGAAGAGGTGGCACCGGTGGCAGGACAAG 1233
QY 1321 CACTCCATCCGTCGCCGAGTGGCCCGTGCATGTCATCCACCTCCCAACCCCGTGC 1380
DB 1234 CACTCGATCCGTCGCCGAGTGGCCCGTGCATGTCATCCCACTCCCAACCCCGTGC 1293
QY 1381 AGTTTTCACAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTGATGGAGAGCCCC 1440
DB 1294 AGTTTTCACAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTGATGGAGAGCCCC 1353
QY 1441 CAAAGAGCTGTGCTGGGGGATGACG 1467
DB 1354 CAAAGAGCTGTGCTGGGGGATGACG 1380

RESULT 12
US-09-799-978-3
; Sequence 3, Application US/09799978
; Patent No. 6670140
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass
; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors
; FILE REFERENCE: 8448
; CURRENT APPLICATION NUMBER: US/09799,978
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 3
; LENGTH: 1285
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (38)..(1285)
US-09-799-978-3

Query Match 75.1%; Score 1188; DB 3; Length 1285;
Best Local Similarity 93.7%; Pred. No. 4.3e-290;
Matches 1285; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 45 CCGGGCATTCAGAGCGTAGCCGAGCGAGCCGCGAGAGTGGAGGGCACCCGAGCTCCG 104
DB 1 CCGGGCATTCAGAGCGTAGCCGAGCGAGCCGCGAGAGTGGAGGGCACCCGAGCTCCG 60
QY 105 TCTCGTCAAGGCCCTTCTCTCTGGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCA 164
DB 61 TCTCGTCAAGGCCCTTCTCTCTGGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCA 120
QY 165 GCATCGGAGAGCTCTCTCTGGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCA 224
DB 121 GCATCGGAGAGCTCTCTCTGGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCA 180
QY 225 GGAACCTCATTTGGCACTGTCTGGCCCGCGAGCCCTGGGGGAGTGTAGTGTTCGGCCCTG 284
DB 181 GGAACCTCATTTGGCACTGTCTGGCCCGCGAGCCCTGGGGGAGTGTAGTGTTCGGCCCTG 240
QY 285 CCTGTCTTTTCTATGGTTCGGCTACATAATCCACAAACAAATGGTGTACCGGAGTGCCT 344
DB 241 CCTGTCTTTTCTATGGTTCGGCTACATAATCCACAAACAAATGGTGTACCGGAGTGCCT 300
QY 345 GGCATATGGAGTGGCCCGCCCGCTGATTAATCTCGAGTGGCAGGAGTCTCTCAATGA 404
DB 301 GGCATATGGAGTGGCCCGCCCGCTGATTAATCTCGAGTGGCAGGAGTCTCTCAATGA 360
QY 405 GGAGAAAAAAGCAAGGTGCACTACCATGTGCGAGTCAATCACTACCTGGGGCACTG 464
DB 361 GGAGAAAAAAGCAAGGTGCACTACCATGTGCGAGTCAATCACTACCTGGGGCACTG 420

RESULT 13

US-09-826-509-482
; Sequence 482, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Lian, Chen W.
; APPLICANT: Lin, I-Lin

QY 465 TATCTCCCTGGTGGCCCTCTCTGGTGGCCCTTGTCTCTCTCTGGGGCTCAGGCCAGGCTG 524
DB 421 TATCTCCCTGGTGGCCCTCTCTGGTGGCCCTTGTCTCTCTCTGGGGCTCAGGCCAGGCTG 469
QY 525 CACCCATTGGGGGTGACACAGCAGATGGAGCCCTGGAGGTGGGGGCTCCATGGAGTGGTGC 584
DB 470 ----- 469
QY 585 CCAATTTCAGGTTCGAAGAGGAGCATCCGGTGCCTGCGAAAAATCATCATCTGGAACCTCAT 644
DB 470 -----AGGAGCATCCGGTGCCTGCGAAAAATCATCATCTGGAACCTCAT 513
QY 645 CTCCGCTTTCATCTCGCGCAAACGCGACCTGGTTCGTGCTCCAGCTAACCATGAGCCGCA 704
DB 514 CTCCGCTTTCATCTCGCGCAAACGCGACCTGGTTCGTGCTCCAGCTAACCATGAGCCGCA 573
QY 705 GGTCCACACAGAGCAACGTCGGGCTGGTGCAGAGTGGTGCAGAGCCGCTTACAACTTTCCA 764
DB 574 GGTCCACACAGAGCAACGTCGGGCTGGTGCAGAGTGGTGCAGAGCCGCTTACAACTTTCCA 633
QY 765 TGTGACCAACTTCTTCTGAGATGTTCCGGGAGGCTGCTACCTGCACACAGCCATCTGTGCT 824
DB 634 TGTGACCAACTTCTTCTGAGATGTTCCGGGAGGCTGCTACCTGCACACAGCCATCTGTGCT 693
QY 825 CACCTACTCCACTGACCGGCTGCGCAATGGAATGTTTCATCTGCTGCTGGCTGGGGTGTGCC 884
DB 694 CACCTACTCCACTGACCGGCTGCGCAATGGAATGTTTCATCTGCTGCTGGCTGGGGTGTGCC 753
QY 885 CTTTCCCATCATTTGTGGCTGGGCTGAGAGTGGTGTGTTTCATCTGCTGCTGGCTGGGGTGTGCC 944
DB 754 CTTTCCCATCATTTGTGGCTGGGCTGAGAGTGGTGTGTTTCATCTGCTGCTGGCTGGGGTGTGCC 813
QY 945 GTTTGGCAAAAGGCTGGGGTGTACACCGACTACATCTACAGGGGCCCAATGATCTGTGT 1004
DB 814 GTTTGGCAAAAGGCTGGGGTGTACACCGACTACATCTACAGGGGCCCAATGATCTGTGT 873
QY 1005 CTGCTGATCAATTTTCATCTCTCTTTTCAACATGCTCCGCTCTCATGACCAAGCTCCG 1064
DB 874 CTGCTGATCAATTTTCATCTCTCTTTTCAACATGCTCCGCTCTCATGACCAAGCTCCG 933
QY 1065 GGCATCCACAGCTCTGAGACCAATTCAGTACAGAAAGGCTGTGAAAGCCACTCTGTGTGT 1124
DB 934 GGCATCCACAGCTCTGAGACCAATTCAGTACAGAAAGGCTGTGAAAGCCACTCTGTGTGT 993
QY 1125 GTTGCCCTCTCTGGGATCACTTACATGCTGTTCTTGTCAATCCCGGGGAGATGAGGT 1184
DB 994 GTTGCCCTCTCTGGGATCACTTACATGCTGTTCTTGTCAATCCCGGGGAGATGAGGT 1053
QY 1185 CTCCGGGTGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1244
DB 1054 CTCCGGGTGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1113
QY 1245 GTCTGTGTTCTACTGTTTCTCAATAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1304
DB 1114 GTCTGTGTTCTACTGTTTCTCAATAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1173
QY 1305 CCGGTGGAGGACCAAGCACTCGATCCGTCGCCGAGTGGGCCCGTGGCCATGTCATCCCCAC 1364
DB 1174 CCGGTGGAGGACCAAGCACTCGATCCGTCGCCGAGTGGGCCCGTGGCCATGTCATCCCCAC 1233
QY 1365 CTCCCCAACCGGTGTCAGCTTTCAGAGTCAAGCATCAAGCATCAAGCATCAAGCATCAAG 1416
DB 1234 CTCCCCAACCGGTGTCAGCTTTCAGAGTCAAGCATCAAGCATCAAGCATCAAGCATCAAG 1285

; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2000-04-07
; PRIOR FILING DATE: 2000-04-07
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 482
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-482

Query Match 72.7%; Score 1149.4; DB 3; Length 1248;
Best Local Similarity 93.4%; Pred. No. 2.4e-280;
Matches 1247; Conservative 0; Mismatches 1; Indels 87; Gaps 1;

QY	82	ATGGGAGGGACCCGAGCTCCGTCTCGTCAAGGCCCTTCTCTCTGCGGCTGGAACCCC	141
DB	1	ATGGGAGGGACCCGAGCTCCGTCTCGTCAAGGCCCTTCTCTCTGCGGCTGGAACCCC	60
QY	142	GTCTCTGCTCCCTCCAGGACCAAGCTGCGAGAGCTGCTCCCTGGCCAGCAATCTCA	201
DB	61	GTCTCTGCTCCCTCCAGGACCAAGCTGCGAGAGCTGCTCCCTGGCCAGCAATCTCA	120
QY	202	GGACTGCGAGTCAACGATCCGCTGAGCACTCATTTGGCACTGCTGGCCCGCAGCCCTGG	261
DB	121	GGACTGCGAGTCAACGATCCGCTGAGCACTCATTTGGCACTGCTGGCCCGCAGCCCTGG	180
QY	262	GGGAGGCTAGTGTGCGGCTGCGGCTGCTTTTCTATGCTGCTGCTGCTGCTGCTGCTG	321
DB	181	GGGAGGCTAGTGTGCGGCTGCGGCTGCTTTTCTATGCTGCTGCTGCTGCTGCTGCTG	240
QY	322	AACAAAGGCTACCGGAGTGGCTGGCCAAATGGCAGCTGGGCGCGCGGCTGGAATCTCC	381
DB	241	AACAAAGGCTACCGGAGTGGCTGGCCAAATGGCAGCTGGGCGCGCGGCTGGAATCTCC	300
QY	382	GAGTGGCAGGAGATCTCTCAATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	441
DB	301	GAGTGGCAGGAGATCTCTCAATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	360
QY	442	ATCATCAACTGCTGGGCACTGTAATCTCTGCTGGGCTGCTCTGCTGGGCTTGTCTCT	501
DB	361	ATCATCAACTGCTGGGCACTGTAATCTCTGCTGGGCTGCTCTGCTGGGCTTGTCTCT	420
QY	502	TTTCTGGGCTCAGGCGAGCTGACCCATTTGGGTTGACCCAGGAGATGGAGCCCTGGAG	561
DB	421	TTTCTGGGCTC-----	432
QY	562	GTGGGGCTCCATGGAGTGGTGCCCATTTTCAGGTTCGAAGGAGCATCCGGTGCCTGGCA	621
DB	433	-----AGGAGCATCCGGTGCCTGGCA	453
QY	622	AACATCATCTGGAACCTCATCTCGCTTTCATCTCGGCAACGCACTGCTGGTGGTG	681
DB	454	AACATCATCTGGAACCTCATCTCGCTTTCATCTCGGCAACGCACTGCTGGTGGTG	513
QY	682	GTCCAGTACCAATGAGCCCGAGGTCCACAGAGCAACGCTGGGCTGCTGAGGTGGTG	741
DB	514	GTCCAGTACCAATGAGCCCGAGGTCCACAGAGCAACGCTGGGCTGCTGAGGTGGTG	573
QY	742	ACAGCCGCTTACAACTCTTCCATGTGACCAACTTCTTCTGGATGTTTCGGCGAGGGCTGC	801
DB	574	ACAGCCGCTTACAACTCTTCCATGTGACCAACTTCTTCTGGATGTTTCGGCGAGGGCTGC	633
QY	802	TACTGCAACAGCATGCTGCTCACTTCACTGACCCGCTGCGCAATGATGATTTTC	861
DB	634	TACTGCAACAGCATGCTGCTCACTTCACTGACCCGCTGCGCAATGATGATTTTC	693

QY	862	ATCTGCAATGGCTGGGCTGGCCCTTCCCATCATTTGTCGCTGGCCCATTTGGAGCTG	921
DB	694	ATCTGCAATGGCTGGGCTGGCCCTTCCCATCATTTGTCGCTGGCCCATTTGGAGCTG	753
QY	922	TACTAGCAATGAGAAGTGTGGTTTGGCAAAAGCCCTGGGGTGTACACCGACTACATC	981
DB	754	TACTAGCAATGAGAAGTGTGGTTTGGCAAAAGCCCTGGGGTGTACACCGACTACATC	813
QY	982	TACCAAGGCCCCATGATCTGCTGCTGATCAATTTTCATCTCTCTTTTCAACATCGTC	1041
DB	814	TACCAAGGCCCCATGATCTGCTGCTGATCAATTTTCATCTCTCTTTTCAACATCGTC	873
QY	1042	CGCATCTCATGACCAAGCTCCGGGCACTCCACACGCTCTGAGACCAATTCAGTACAGGAAG	1101
DB	874	CGCATCTCATGACCAAGCTCCGGGCACTCCACACGCTCTGAGACCAATTCAGTACAGGAAG	933
QY	1102	GCTGTGAAAGCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1161
DB	934	GCTGTGAAAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	993
QY	1162	GTCATCCCGGGAGGATGAGTCTCCCGGGTGGTCTTCTCATCTTCACTTCACTTCTTCTG	1221
DB	994	GTCATCCCGGGAGGATGAGTCTCCCGGGTGGTCTTCTCATCTTCACTTCACTTCTTCTG	1053
QY	1222	GATCTCTCAGGGCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1281
DB	1054	GATCTCTCAGGGCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1113
QY	1282	TCTGCCATCCGAAGAGTGGCAACGGTGGGAGGCAAGCACTTCGATCCGTCGCGAGTG	1341
DB	1114	TCTGCCATCCGAAGAGTGGCAACGGTGGGAGGCAAGCACTTCGATCCGTCGCGAGTG	1173
QY	1342	GCCGTCGATGTCATCCCACTCCCAACCGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1401
DB	1174	GCCGTCGATGTCATCCCACTCCCAACCGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1233
QY	1402	TCCACAGCAGTCTGA	1416
DB	1234	TCCACAGCAGTCTGA	1248

RESULT 14
US-09-799-978-7
; Sequence 7, Application US/09799978
; Patent No. 6670140
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or
; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors
; FILE REFERENCE: 8448
; CURRENT APPLICATION NUMBER: US/09/799,978
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 1206
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1206)
US-09-799-978-7

Query Match 66.8%; Score 1057; DB 3; Length 1206;
Best Local Similarity 90.3%; Pred. No. 5.1e-257;
Matches 1206; Conservative 0; Mismatches 0; Indels 129; Gaps 2;
QY 82 ATGGGAGGGACCCGAGCTCCGTCTCGTCAAGGCCCTTCTCTCTTCTGGGGCTGAACCCC 141
DB 1 ATGGGAGGGACCCGAGCTCCGTCTCGTCAAGGCCCTTCTCTCTTCTGGGGCTGAACCCC 60

142 GTCTCTGCTCCCTCCAGGACCGAGCTCGAGAGCCTGTCCCTGGCCAGCAATCTCA 201
Db
61 GTCTCTGCTCCCTCCAGGACCGAGCTCGAGAGCCTGTCCCTGGCCAGCAATCTCA 120
QY 202 GGACTGCACTGCAACGCACTCGTGAGACTCAATGGCACTGCTGGCCCGCCAGCCCTGCG 261
Db 121 GGACTGCACTGCAACGCACTCGTGAGACTCAATGGCACTGCTGGCCCGCCAGCCCTGCG 180
QY 262 GGGAGCTAGTGGTTGGCCCTGCGCTGCTGCTTTTCTATGGTTCGCTACATACACA 321
Db 181 GGGAGCTAGTGGTTGGCCCTGCGCTGCTGCTTTTCTATGGTTCGCTACATACACA 240
QY 322 AACATGGCTACCGGAGTGCCTGGCAATGGAGCTGGCCCGCCGCGTGAATTAATCC 381
Db 241 AACATGGCTACCGGAGTGCCTGGCAATGGAGCTGGCCCGCCGCGTGAATTAATCC 300
QY 382 GAGTGCAGGAGATCCTCAATGAGGAGAAAAAGCAAGGTGCACTACCATGTGCGAGTC 441
Db 301 GAGTGCAGGAGATCCTCAATGAGGAGAAAAAGCAAGGTGCACTACCATGTGCGAGTC 360
QY 442 ATCATCAACTACCTGGGCCA CTGTAATCTCCTGGTGGCCCTCTCTGTGGCTTTGCTTC 501
Db 361 ATCATCAACTACCTGGGCCA CTGTAATCTCCTGGTGGCCCTCTCTGTGGCTTTGCTTC 420
QY 502 TTTCTGGGCTCAGGCCAGGCTGCA CCCATTGGGTTGACCCAGGAGATGAGCCCTGGAG 561
Db 421 TTTCTGGGCTC----- 432
QY 562 GTGGGGCTCCATGGAGTGTGGCCCAATTTTCAGGTTGCAAGGAGATCCGGTGCCTGGCA 621
Db 433 -----AGGAGCATCCGGTGCCTGGCA 453
QY 622 AACATCACTGGAACCTCATCTCGCCTTCACTGCGCAACGCACTCGTTGCTG 681
Db 454 AACATCACTGGAACCTCATCTCGCCTTCACTGCGCAACGCACTCGTTGCTG 513
QY 682 GTCCAGTACCAATGAGCCCGAGGTCCACGAGCAACCTGCGGTGCTGAGTGGTG 741
Db 514 GTCCAGTACCAATGAGCCCGAGGTCCACGAGCAACCTGCGGTGCTGAGTGGTG 573
QY 742 ACAGCGCCTACCACTCTCATGTGACCAACTTCTTGGATGTTGCGCGAGGCTGC 801
Db 574 ACAGCGCCTACCACTCTCATGTGACCAACTTCTTGGATGTTGCGCGAGGCTGC 633
QY 802 TACTGCAACAGCCATCGTGCTCACTACTCACTGACCGGCTGCGCAATGATGTT 861
Db 634 TACTGCAACAGCCATCGTGCTCACTACTCACTGACCGGCTGCGCAATGATGTT 693
QY 862 ATCTGCAATGGCTGGGCTGCTGCTTCCCATCATGTTGGCCTGGGCCATTTGGAGCTG 921
Db 694 ATCTGCAATGGCTGGGCTGCTGCTTCCCATCATGTTGGCCTGGGCCATTTGGAGCTG 753
QY 922 TACTGCAACAGAGTCTGCTGTTTGGCAAGGCTGCGGTTGACCGACTACATC 981
Db 754 TACTGCAACAGAGTCTGCTGTTTGGCAAGGCTGCGGTTGACCGACTACATC 813
QY 982 TACCAGGCCCCATGATGCTGCTGCTGATCAATTTCTCTTTTCAACATGCTC 1041
Db 814 TACCAGGCCCCATGATGCTGCTGCTGATCAATTTCTCTTTTCAACATGCTC 873
QY 1042 CGCATCTCATGACCAAGCTCGGGCATTCACACAGTCTGAGACCATTCAGTACAGGA 1101
Db 874 CGCATCTCATGACCAAGCTCGGGCATTCACACAGTCTGAGACCATTCAGTACAGGA 933
QY 1102 GCTGTGAAGCCACTCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1161
Db 934 GCTGTGAAGCCACTCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 993
QY 1162 GTCAATCCCGGGAGGATGAGGCTCTCCGGGCTGCTTCTTCACTTCACTTCTTCTG 1221
Db 994 GTCAATCCCGGGAGGATGAGGCTCTCCGGGCTGCTTCTTCACTTCACTTCTTCTG 1053
QY 1222 GAATCTCTCCAGGGCTTTCTTGTGTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCT 1281

Db 1054 GATCTCTTC-----AGGTCCGT 1071
QY 1282 TGTGCCATCCGAAGAGTGGCACCGGTGGCAGACAAGCACTCGATCCGTGCCAGTG 1341
Db 1072 TGTGCCATCCGAAGAGTGGCACCGGTGGCAGACAAGCACTCGATCCGTGCCAGTG 1131
QY 1342 GCGCGTGCATGTCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCC 1401
Db 1132 GCGCGTGCATGTCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCC 1191
QY 1402 TCCACAGCAGTCTGA 1416
Db 1192 TCCACAGCAGTCTGA 1206
RESULT 15
US-08-482-746-5
; Sequence 5, Application US/08482746B
; Patent No. 6399315
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; FILE REFERENCE: P41-90002
; CURRENT APPLICATION NUMBER: US/08/482,746B
; CURRENT FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: US 08/374,009
; EARLIER FILING DATE: 1995-01-17
; EARLIER APPLICATION NUMBER: US 08/353,537
; EARLIER FILING DATE: 1994-12-09
; EARLIER APPLICATION NUMBER: PCT/US94/05908
; EARLIER FILING DATE: 1994-05-25
; EARLIER APPLICATION NUMBER: US 08/110,286
; EARLIER FILING DATE: 1993-08-23
; EARLIER APPLICATION NUMBER: US 08/079,320
; EARLIER FILING DATE: 1993-06-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1411
; TYPE: DNA
; ORGANISM: Rattus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (80)...(1324)
US-08-482-746-5
Query Match 65.4%; Score 1035.2; DB 3; Length 1411;
Best Local Similarity 83.8%; Pred. No. 1.7e-251;
Matches 1258; Conservative 0; Mismatches 153; Indels 91; Gaps 4;
QY 3 AGCCCGCAGCGCCCGCCCGCTTCTCTGGGATGTCCTGAGACCCCGGCAATTCAGGACGG 62
Db 1 AGACCGCAGCGCCCGCCCGCTTCTGGGATGTCGAGGCGATCCAGGATCCAGGACGC 60
QY 63 TAGCCGAGGAGCCCGGAGGATGGAGGCGCACCCGAGCTCCGTCTGTCGTAAGGCCCTTCT 122
Db 61 TGACGAGGAGCCCGGAGGATGGAGGCGCGCCCGAGCTCCGGCTCGTGAAGGCCCTTCT 120
QY 123 CCTTCTGGGCTGAACCCCGCTCTCTGCTCCCTCCAGGACCGACACTGCCAGAGCCCTGTC 182
Db 121 CCTTCTGGGCTGAACCCCGCTCTCTGCTCCCTCCAGGATCAGGCTGTGAGAACCTGTC 180
QY 183 CCTGGCCAGCAACATCTCAGGACTGCAAGTGCACAGCATCCGTGGACCTCATTTGGCACCTG 242
Db 181 CCTGACCAACGATGTTTCTGGCCTGCAATGCAATGCAATCCGTGACCTCATTTGGCACCTG 240

Qy 243 CTGCGCCCGCAGCCCTGCGGGCAGCTAGTGGTTGCGCCCTGCGCCTCTTTTCTATGG 302
Db 241 CTGCGCCCGGAGCCCTGCGGGCCAGTTGGTGGTCGAGCCCTGCGCCTTTTCTACGG 300
Qy 303 TGTCCGCTACAATACACAAACAAATGGCTACCGGGAGTGTCTGGCCAAATGGCAGCTGGGC 362
Db 301 TGTCCGCTACAACACACAAACAAATGGCTACCGGGAGTGTCTGGCCAAACGGCAGCTGGGC 360
Qy 363 CGCCCGGCTGAATTTACTCCGAGTGCCAGGAGATCTCAATGGAGGAGAAAAGCAAGGT 422
Db 361 AGCCCGGTGAATTAATTTCTGAGTGCCAGGAGATCTCAAGAGAGAGAAAGCAAGGT 420
Qy 423 GCACCTACATGTGCGAGTCAATCAATCACTACCTGGGCCACTGTATCTCCCTGTGGCCCT 482
Db 421 ACACCTACCATGTTGCACTCATCACTCACTACCTGGGTCACTGCATCTCCCTGTGGCCCT 480
Qy 483 CTTGTGGCCCTTTGTCTCTTTCTGGGCTCAAGGCCAGGCTGCACCCATTTGGGGTGACCA 542
Db 481 CTTGTGGCCCTTTGTCTCTCTTTCTGGGCTC----- 511
Qy 543 GGCAGATGGAGCCCTGGAGGTGGGGGCTCCATGGAGTGGTGGCCCATTTTCAGGTTCGAAG 602
Db 512 -----AG 513
Qy 603 GAGCATCCGGTGTCTGCGAAACATCACTGGAACCTCATCTCGGCCCTTCACTCCTGGC 662
Db 514 GAGCATCCGGTGTCTGAGAAACATCACTGGAACCTCATCTCGGCTTTCACTCCTAGC 573
Qy 663 CAACGGCACCTGGTTGGTGTCCAGCTAACATGAGCCCGAGGTCCACAGAGCAACGT 722
Db 574 CAACGGCACCTGGTTGGTGTCCAGCTCAACGTGAGCCCGAGGTGCAACAGAGCAATGT 633
Qy 723 GGGCTGGTCAGAGTGGTGGACCGGCTCACTACTTCCATGTGACCAATCTTCTCTG 782
Db 634 GGGCTGGTGTAGGTGGTGGACCGGCTCACTACTTCCATGTGTAACCAATCTTCTCTG 693
Qy 783 GATGTTCCGGGAGGGCTGTACTGTGCACACAGCCATCGTGTCTCACTCTCACTGACCG 842
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Qy 1023 CTTCCCTTTTCAATCGTCCGCATCTCTATGACCAAGCTCCGGGCATTCACCAAGCTGTA 1082
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Qy 1083 GACCATTCAGTACAGGAGGCTGTGAAGGCACTCTGTGTCTGTGCTGCTGCTGCTGGGCAT 1142
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Db 1294 CTTTTCACAGCATCAAGCAGTCCACAGCAGTGTGAGCT-CCAGGCCACAGAGCAGCCCCC- 1351
Qy 1443 AAGAGCTGTGGCTGGGGGATGACGGCCAGGCTCCCTGACCACTTGCCTGTGGAGTCA 1502
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Qy 1503 CC 1504
Db 1410 GC 1411

Search completed: March 17, 2006, 10:59:06
Job time : 395 secs

Result No.	Query			Description	
	Score	Match	Length	DB	ID
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2	545	34.5	1626	12	US-11-136-527-2713
3	464.2	29.3	600	12	US-11-136-527-6936
4	286.2	18.1	600	12	US-11-136-527-6809
5	144.8	9.2	1400	12	US-11-136-527-6986
6	144.8	9.2	1815	12	US-11-136-527-2890
7	134.2	8.5	5192	12	US-11-136-527-2085
8	129.6	8.2	3066	12	US-11-136-527-3765
9	128.4	8.1	3453	12	US-11-136-527-1893
10	124.6	7.9	3434	12	US-11-136-527-1894
11	124	7.8	613	6	US-09-925-065A-506766
12	120.2	7.6	1806	12	US-11-136-527-4065
13	115.4	7.3	2065	12	US-11-136-527-2547
14	98	6.2	2786	12	US-11-128-061-870
15	98	6.2	2786	12	US-11-128-049-870
16	92.4	5.8	2715	12	US-11-136-527-2059
17	90.4	5.7	2121	12	US-11-136-527-3511
18	90	5.7	1977	12	US-11-136-527-2881
19	79.2	5.0	1640	9	US-11-245-147-163
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/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (341)..(342)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (500)..(501)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (535)..(540)
/ OTHER INFORMATION: n is a, c, g, or t
US-11-136-527-2840

Query Match      64.4%; Score 1019.2; DB 12; Length 2044;
Best Local Similarity 81.1%; Pred. No. 7.2e-247;
Matches 1210; Conservative 46; Mismatches 145; Indels 91; Gaps 4;

QY      2  GAGCCGACGCGCCCGGTTCTCTGGGATGTCCGTAGGACCCGGGCAATTCAGGACG 61
DB      643 GAGACCGACGCGCCCGCTCCGCTCTGGGATGTCCGAGGATCCAGGCAATCCAGGACG 702

QY      62  GTAGCGAGCGAGCGCGAGGATGGAGGACCCGCGAGCTCCGTCTGTCGTAAGGCCCTTC 121
DB      703 CTGACGAGCGAGCGCGAGGATGGAGGACCGCGCGAGCTCCGRCYCSYRMAGGYMMKWC 762

QY      122 TCCTCTGGGGTGAAACCCCGTCTCTGCCCTCCAGGACCAAGCACTGGAGAGCTGT 181
DB      763 TCCTCTGGGGTGAAACCCCTGTCTCCACCTCCCTTCAGGATCAGCGCTGTGAGAACCTGT 822

QY      182 CCCTGGCCAGCAACATCTCAGGACTGTCAGTGCACGATCCGTGGACCTCATTTGGCACT 241
DB      823 CCCTGGACGACATKTYCTGGCTTCGAGTGCAATGCATCCGTGGACCTCATTTGGCACT 882

QY      242 GCTGGCCCCGAGCCCTGCGGGGAGCTAGTGTGTGGCCCTGCGCTGCTTTTCTATG 301
DB      4883 GCTGGCCCCGAGCCCTGCGGGGCACTGTGGTGGTCCGACCTGCGCTGCTTTTCTACG 942

QY      302 GTCTCGCTACAATACACAAACATGGCTACCGGAGTGCTGGCCAAATGGCAGCTGGG 361
DB      943 GTGTGGCTACAACACAAATGAAGRMATACCGGAGTGCTGGCCAAATGGCAGCTGGG 1002

QY      362 CGCCCGCGTGAATTAATCCGAGTGCCAGGAGATCTCAATGAGGAGAAAAAGCAAGG 421
DB      1003 CAGCCCGTGTGAATTAATTCGAGTGCCAGGAGATCTCAACGAGAGAGAGCAAG 1062

QY      422 TGCACTACCAATGTCGAGTCAATCACTACCTGGGCACTGTATCTCCTGGTGGCCC 481
DB      1063 TACACTACCAATGTCGAGTCAATCACTACCTGGGCACTGTATCTCCTGGTGGCCC 1122

QY      482 TCCTGGTGGCTTTGTCCTCTTCTGCGCTCAGGCCAGGCTGCACCCATTTGGGTGACC 541
DB      1123 TCCTGGTGGCTTTGTCCKMKKYTGGSCTCAGK----- 1157

QY      542 AGGCAGATGAGCCCTGGAGGTGGGGCTCCATGAGGTGGTGGCCCATTTTCAGGTTCGAA 601
DB      1158 ----- 1157

QY      602 GGAGATCCGGTGCCTGCGAAACATCATCACTGGAACCTCATCTCGCCTTCATCTGTC 661
DB      1158 --AGCATCCGGTGCCTGAGAAACATCATCACTGGAASCTCATCTCGGCTTTTCATCTAC 1215

QY      662 GCAACGCCACCTGGTTGGTTCAGTACCAATGAGCCCGGAGGTCCACGAGCAACG 721
DB      1216 GCAACGCCACCTGGTTGGTTCAGTACCAATGAGCCCGGAGGTCCACGAGCAACG 1275

QY      722 TGGGCTGGTGCAGGTGGTGCAGCGGCTTCACTTCCATGTGACCAACTTCTTCT 781
DB      1276 TKGBCWGTGTAGTGGTGCAGACCGGCTTCACTTCTTCAATGTAACAACTTCTTCT 1335

QY      782 GATGTTGGCGAGGGTGTCTGACACAGCCATCGTGTCTCACTTCCATCCATGACC 841
DB      1336 GGATGTTGGTGGGGTGTCTGACACAGCCATTTGTGCTCACTTCCACCGACC 1395
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QY      842 GGCTGCGCAAAATGAGTGTTCATCTGCAATTTGGCTGGGGTGTGCCCTTCCCATCATTTGTGG 901
DB      1396 GTCTGCGCAAGTGGATGTTCGCTGCAATTTGGCTGGGGTGTASCTKKSCCCATCATTTGTGG 1455

QY      902 CTTGGGCCAATTTGGGAAGCTGTACTACGACAATAGAAAGTGTGGTTTGGCAAGGCTGTG 961
DB      1456 CTTGGGCCAATTTGGGAAGCTGTACTACGACAATAGAAAGTGTGGTTTGGCAAGGCTGTG 1515

QY      962 GGGGTACACCGACTACATCTACAGGGGCCCATGATCTCGTCTGCTGCTGATCAATTTCA 1021
DB      1516 GGGTATACACCTGACTACATCTACAGGGGCCCATGATCTCGTCTGCTGCTGATCAATTTA 1575

QY      1022 TCTTCTCTTTCAACATCGTCCGCATCTCATGACCAAGCTCCGGGATCCACCAAGCTGTG 1081
DB      1576 TCTTCTCTTTCAACATCGTCCGCATCTCATGACCAAGCTCCGGGATCCACCAAGCTGTG 1635

QY      1082 AGACCAATTCAGTACAGAAAGGCTGTGAAAGCCACTCTGTGTGTGCTGCTGCTCTGGGCA 1141
DB      1636 AGACCAATTCASVYAGGAAGGCTGTGAAAGCCACTCTGTGTGTGCTGCTGCTCTGGGCA 1695

QY      1142 TCACCTACATGCTGTTCTTGTTCATCCCGGGGAGGATGAGGTCTCCGGGTGCTCTTCA 1201
DB      1696 TCACCTACATGTTGTTCTTGTTCATCCCGGGGAGGATGAGGTCTCCGGGTGCTCTTCA 1755

QY      1202 TCTACTTCAACTCTCTCTGGAATCTTCCAGGGCTTCTTGTGTGCTGTGTGTCTACTGTT 1261
DB      1756 TCTACTTCAACTCTTCTTGTGAGTCTTTCAGGRCYCTTGTGTGCTGTGTGTCTACTGTT 1815

QY      1262 TCCTCAATAGTGAAGTCCGTTCTGCCATCCGGAAGAGGTGGCACCGGTGGCAGCAAGC 1321
DB      1816 TTTGTMRONGYAGGCTCCGCTCGCTATCCGGAAGAGGTGGCGTCCGTGGCAGCAAGC 1875

QY      1322 ACTCGATCCGTCGCCGAGTGGCCCGTGCATGTCATCCCACTCCCAACCCGTGTCA 1381
DB      1876 ACTCCATCAGAGCCGAGTGGCCCGGAGTATGTCTCATCCCACTCCCAACCCGTGTCA 1935

QY      1382 GCTTTCACAGCATCAAGCAGTCCACAGCAGTCTGAGCTGCGAGGTCAATGAGCAGCCCC 1441
DB      1936 GCTTTCACAGCATCAAGCAGTCCACAGCAGTCTGAGCT--CAGGCCACAGAGAGCCCC 1994

QY      1442 AAGAGCTGTGGCTGGGGGATGACCGCCAGGCTCCCTGACCAACCCCTGCTG 1493
DB      1995 --AAGACTGAGGCCGGGAGATGATG--CAAGCTCACTGACGAGCAGTCTG 2043

RESULT 2
US-11-136-527-2713
; Sequence 2713, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2713
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2713

Query Match      34.5%; Score 545; DB 12; Length 1626;
Best Local Similarity 67.9%; Pred. No. 1.8e-127;
Matches 854; Conservative 0; Mismatches 310; Indels 93; Gaps 3;

QY      165 GCATCGGAGAGCTGTCCCTGGCCAGCAACATCTCAGGACTGCACTGCAACGATCCGT 224
```


Db 287 GGACGGCTGGGAGAGCCCGGACCCGAGGTCCCTACTCTCTGCAACAGACCTT 346
Qy 225 GGAACCTCATTTGGGCACTGCTGGCCCCGACGCCCTGGGGGAGAGTAGTGTTCGGCCCTG 284
Db 347 GGACCAATCGGAGACCTGCTGGCCCCAGAGCGGCCCTGGAGCCCTAGTGAGAGACCATG 406
Qy 285 CCCTGCTTTTCTATGGTGTCCGCTACAAATACCAACAAAGTGGCTACCGGAGTGCCT 344
Db 407 CCCGGAATCTTCAACGGCATCAAGTACAAACAGACCCGGAATGCCTTACAGAAATGCCT 466
Qy 345 GGCAATGGCAGCTGGGCCCCCGCGCTGAATTAATCTCCGAGTGGCAGGAGATCCTCAATG- 403
Db 467 GGAGATGGACCTGGGCTCAAGGATCACTACTCACTGTGNAACCAATTTGGATGA 526
Qy 404 --AGGAGAAAAAGCAAGGTGCACTACCATGTGCGAGTCAATCACTAACTACTCTGGGCCA 461
Db 527 CAAGCAGAGGAATATGACCTGCAATACCGAATCGCCCTCATCACTAACTACTCTGGGCCA 586
Qy 462 CTGTATCTCCCTGCTGGCCCTCTGGTGGCTTGTCTCTCTTCTGGGCTCAGGCCAGG 521
Db 587 CTGTGTTCCGTGGTGGCCCTGGTGGCTGCTTCTCTGCTTTTCTCT----- 631
Qy 522 CTCACCCATTGGGGTGACCAAGCAGATGAGGCCCTGGAGGTGGGGCTCCATGAGTGG 581
Db 632 ----- 631
Qy 582 TGCCCCATTTCAAGTTGGAAGGAGATCCGGTGGCTTGGAAACATCATCACTGGAACT 641
Db 632 -----AGTGTGGGGAGTATCCGCTGCTGCGGAATGTGATCCACTGGAACT 679
Qy 642 CATCTCGCTTCTCTGCGCAACGCCACCTGGTGGTGGTCCAGCTAACCATGAGCCC 701
Db 680 CATCACACCTTCTCTGAGAAACATCACTGGTGGTGGTCTCTGCTGCACT---CATGACCA 736
Qy 702 CGAGGTCCACACAGCAACCTGGGCTGGTGCAGGTGGTGGACAGCCGCTTACAACTACTT 761
Db 737 CGAAGTGCAAGGGGCAATGAGTCTGGTGGCTGGCTGCTGCACTATTTCACTACTT 796
Qy 762 CCAATGACCAACTTCTTCTGGATGTTGGCGAGGGCTGTACTGCAACAGCCATCGT 821
Db 797 TGTGGTCAACCACTTCTTCTGGATGTTGTGGAAGGCTGTACTGCAACAGCCATCGT 856
Qy 822 GCTCACTACTTCACTGACCGGCTGGCAATGGATGTTCACTGCAATTTGGCTGGGGTGT 881
Db 857 CATGAGCTACTCACGAGCATCTGGCAAGTGGCTCTTCTCTTCAATTTGGATGGTGCAT 916
Qy 882 GCCCTTCCCATCAATTTGTGGCTGGGCAATGGAGAGCTGTACTACGACAACTGAGAAGTG 941
Db 917 ACCCTGGCTATCAATTTGTGCGCTGGGCAATGGAGAGTGGCAAACTCTACTATGAGAAAGCAGTG 976
Qy 942 CTGGTTTGGCAAGGCTGGGGTGTACACCGACTACATCTACAGGGGCCCCATGATCCT 1001
Db 977 CTGGTTTGGCAAGGACCTGGTGAATTTAGTGGACTACATCTACAGGGGCCCATCATCCT 1036
Qy 1002 GGTCTGCTGATCAATTTCTATCTTCTTTTCAATGCTGGCATCTCGATGCAAGACT 1061
Db 1037 CGTCTCTCTCATCAATTTTGTGTTCTGTTTCAACATCTGTGAGATCTGTATGCAAACT 1096
Qy 1062 CCGGGCATCCACAGCTCTGAGACCAATTCAGTACAGAGGCTGTGAAAGCCACTCTGTT 1121
Db 1097 GCGAGCTTCCACCAATCCGAGACCATCCAGTACAGAGGAGTGAAGGCCACCTCTGTT 1156
Qy 1122 GCTGCTGCCCTCTCTGGGCACTCACTACATGCTGTTCTTCTGTCATCCCGGGGAGGATGA 1181
Db 1157 CCTCTCTCTCTGTTGGGCACTCACTTACATGCTCTTCTTGTCAATCTCTGGAGGACGA 1216
Qy 1182 GGTCTCCGGGCTGCTCTTCACTACTTCACTCTCTCTCTGGAATCTCTTCCAGGGCTTCTT 1241
Db 1217 CTGTGACAGATTTGTCTACTACTTCACTCTTCTCTGAGTCTCTTCTGAGGTTTCTT 1276
Qy 1242 TGTGCTGTTGTTCTACTGTTTCTCAATAGTGAAGTCCGTTCTGCAATCCGGAAGGTTG 1301
Db 1277 TGTGCTGTTTCTACTGCTTCTCAATAGGAGGTTGCGCTCCGCTCTGAGAAAGCGGTG 1336

Qy 1302 GCACCGGTGGCAGGCAAGCACTCGATCCGTGCCCGAGTGGCCGTCGATGTCCATCC 1361
Db 1337 GCACCGTTGGCAGGACCAACCAAGCCCTCCGAGTGCCTGTGGCCCGGCGCATGTCCATTC 1396
Qy 1362 CACTCCCCAACCCGCTGTCAGCTTTTCCAGCATCAAGCAGTCCACAGCAGCTCTGAGC 1418
Db 1397 CACATGCCACCACCGATCAGCTTCCACAGCATCAAGCAGCAGCTGCCGTGTGATC 1453

RESULT 3
US-11-136-527-6936
; Sequence 6936, Application US/111136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6936
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-6936

Query Match 29.3%; Score 464.2; DB 12; Length 600;
Best Local Similarity 87.4%; Pred. No. 3.3e-107;
Matches 527; Conservative 12; Mismatches 60; Indels 4; Gaps 3;
Qy 891 CATCATTTGGCTGGCCATTTGGGAAGCTGTACTACGACAAATGAGAAGTGTGTTGG 950
Db 1 CATCATTTGGCTGGCCATTTGGGAAGCTGTACTACGACAAATGAGAAGTGTGTTGG 60
Qy 951 CAAAGGCCCTGGGGTGTACACCGACTACATCTACAGGGGCCCATGATCCTGCTCTGCT 1010
Db 61 CAAAGGCCCTGGGGTGTACATGACTACATCTACAGGGGCCCATGATCCTGCTCTGCT 120
Qy 1011 GATCAATTTCACTTCTCTTTTCAACATCGTCCGCACTCTCATGACCAAGCTCCGGGATC 1070
Db 121 GATCAATTTTATCTTCTTCTTCAACATTTGCGCATCTCTCATGACCAAACTCCGGGATC 180
Qy 1071 CACCAGCTCTGAGACCAATTCAGTACAGGAAGGCTGTGAAGCCACTCTGCTGCTGCC 1130
Db 181 CACTACATCTGAGACCAATTCASWYAGGAAGGCTGTGAAGGCCACTCTGCTGCTGCC 240
Qy 1131 CCTCTGGGCATCACCTACATGCTGTTCTTTCGTCATCTCCGGGAGGATGAGGTCTCCCG 1190
Db 241 CCTCTGGGCATCACCTACATGTTGTTCTTTCGTCACCCCTGGAGAGGACGAGGTCTCCAG 300
Qy 1191 GGTGCTTCTCATCTACTCAATCTCTTCTCTGGAATCTCTTCCAGGGCTTCTTGTGTGT 1250
Db 301 GGTGCTTCTCATCTACTCAACTCTTCTTCTGAGTCTCTTTCAGGRCYTCYTTGTGTGT 360
Qy 1251 GTTCTACTGTTTCTCAATAGTGAAGTCCGTTCTGTCATCTCCGGAAGGTTGGCACCGGTG 1310
Db 361 GTTCTACTGTTTCTWRCMGYAGGTCGCTCCGCTATCCGGAAGGTTGGGTGCGGTG 420
Qy 1311 GCAGGACAAAGCACTCGATCCGTCGCGAGTGGCCCTGTCATCTCATCCCACTCCCTCCC 1370
Db 421 GCAGGACAAAGCACTCCATCAGAGCCGAGTGGGCCGAGCTATGTTCATCCCACTCCCTCCC 480
Qy 1371 AACCCGCTGTCAGCTTTTCAAGCATCAAGCAGTCCACAGCAGTCTGAGCTGCGAGGTCATG 1430
Db 481 GACCAAGTCTGCTTTTCAAGCATCAAGCAGTCCACAGCAGTGTGAGCT--CCAGGGCCACA 539
Qy 1431 GAGCAGCCCAAGAGCTGTGCTGGGGGATGACGGCCAGGCTCCCTGACCACTGTC 1490

QY	1304	ACCGTGGCGAGGACAAGCACTCGATCCGTGCCCGAGTGGCCCGTGCATGTCATGCCCA	1361
Db	1423	GCCAGTGGCACTTCAAGAGTTCCTCCGCTGCGCCCTGTGGCCCTTCAATACTCTCTTACGA	1482
QY	1364	CTCTCCCAACCCCGTGTCAAGCTTTTCACAGCA	1393
Db	1483	ACGCCACCAACGGCCCAACCCACAGCACCA	1512
RESULT 7			
US-11-136-527-2085			
; Sequence 2085, Application US/11136527			
; Publication No. US20050287570A1			
; GENERAL INFORMATION:			
; APPLICANT: Wyeth			
; APPLICANT: Mounts, William M			
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes			
; FILE REFERENCE: 031896-041000 (AM101086)			
; CURRENT APPLICATION NUMBER: US/11/136,527			
; CURRENT FILING DATE: 2005-05-25			
; PRIOR APPLICATION NUMBER: US 60/574,294			
; PRIOR FILING DATE: 2005-05-26			
; NUMBER OF SEQ ID NOS: 362830			
; SOFTWARE: PatentIn version 3.2			
; SEQ. ID NO 2085			
; LENGTH: 5192			
; TYPE: DNA			
; ORGANISM: Rattus norvegicus			
US-11-136-527-2085			
Query Match 8.5%; Score 134.2; DB 12; Length 5192;			
Best Local Similarity 54.2%; Pred. No. 6.3e-24;			
Matches 396; Conservative 0; Mismatches 308; Indels 27; Gaps 5;			
QY	601	AGGAGCATCCGGTGCCTGCGAAACATCATCCACTGGAACTCATCTCCGCTTTCATCTG	660
Db	2626	AGGAAGCTGCACGTGTACCCGAAACTACATCCACATGCACTCTTTCATGTCTTTCATCTG	2685
QY	661	CGCAACGCCACCTGGTTC-----GTGGTCCAGCTAACCATGATGACCCCGAGGTCCACCAG	714
Db	2686	AGGGCCACTGCCGTCTTCATCAAGGACATGGCCCTCTTCAACACGCGGGAGATAGACCAC	2745
QY	715	AGCAACGTGGGCT-----CGTGAGGTGGTGACAGCCGCTTCAACTACTTCCATGTG	768
Db	2746	TGCTCTGAGGCTCGGTGGGTGCAAGGACGGTGGTTTCTTCCAGTATTTGTGTATG	2805
QY	769	ACCAACTTCTTCTGGATGTTTCGCGAGGGTGTACTGTGCACACAGCCATCGTGTCTCACC	828
Db	2806	GCCAACTTCTTCTGGCTGTGTGGTAGAGGGCTCTACCTATACACCTGTGGCGGTCTCC	2865
QY	829	TACTCACTGACCGGCTGCCAAATGGATGTTTATCTGTGATTTGGCTGGGGTGTGCCCTTC	888
Db	2866	TTCTTCTCCAGCGGAAGTACTTCTGSGGGGTACATCTCATCGCTGGGGAGTGCACAGT	2925
QY	889	CCCATCAATTGCGCTGGGGCAATTGGGAAGCTGTACTACGACAATAGAAAGTCTGTGTT	948
Db	2926	GTGTTTATACCATATGGAACGGTCTGCAGATATATTTTGAGGATTTTCGGGTGCTGG---	2982
QY	949	GGCAAAAGGCTTGGGTGTATACCCGACTACATTTACAGGGGCCCATGATCTCTGGTCTG	1008
Db	2983	GACACCATCAATCACTCTCCCTGTGTGTGATCATAAAGGCCCCCATCTCTCTCTCCATC	3042
QY	1009	CTGATCAATTTCACTCTCTTTTCAACATCGTCGGATCTCTATGACCAAGCTCCGGGCA	1068
Db	3043	CTGGTGAACATTCTGCTCTGTTTATCTGTCATATCCGGATCTCTGGTTTCAAGAACTACGGCC	3102
QY	1069	TCCACC-----ACGTCTGAGACCATTCAGTACAGGAAGGCTGTGAAAGCCACTCTGGT	1122
Db	3103	CCCGACATTTGGGAAGATGATAGCAGCCCATATTCGAGGCTGGCCAAAGTCCACGCTTCTG	3162
QY	1123	CTGCTGCCCTCTCTGGGCATCACTCATGCTGTTTCTGTTCTAATCCGGGGAGGATGAG	1182

Db 3163 CTCATCCCTGTTGGAAATTCATATGTTGGCTTCTTCCCGCAAACTCAAG 3222
QY 1183 GTCTCCGGGTGCTTCACTACTTCACTCTTCTTGGAAATCCTTCCAGGGCTCTTT 1242
Db 3223 GCCAG-----GTGAAATGGCTTTCGAACTTGTGTGGGCTCTTTCAGGGTTCGTG 3276
QY 1243 GTGTCTGTGTCTACTGTTTCTTCAATAGTAGAGTCCGTTCTGCCATCCCGAAGAGGTGG 1302
Db 3277 GTGGCCATCTCTACTGTTCTTCAATGTTGAGGTGACAGCGGAGCTGCGCGGAAGTGG 3336
QY 1303 CACCGGTGGCA 1313
Db 3337 CGCGTTGGCA 3347

RESULT 8

US-11-136-527-3765
; Sequence 3765, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3765
; LENGTH: 3066
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3765

Query Match 8.2%; Score 129.6; DB 12; Length 3066;
Best Local Similarity 52.0%; Pred. No. 8.2e-23;
Matches 344; Conservative 0; Mismatches 309; Indels 9; Gaps 2;
QY 728 GTGCGAGTTGGTGACAGCGCTTACAACTACTTCCATGACAACTTCTTCTGAGT 787
Db 690 GCTGCGGACTGGTGTCTCTCTCATGCAATACTGCGTGGCGGCAACTACTACTGTTGC 749
QY 788 TCGCGAGGCTGCTACTTCCACAGCCATCTGTCTCACTACTCACTGACGGCTGC 847
Db 750 TGTGGAAGCGGTATCTGTATACACTGCTGCTCTCTCGGTCTCTCGGAGCGCA 809
QY 848 GCAATGGATGTTTCATCTGCAATGGCTGGGCTGTGCCCTTCCCATCATTTGTGGCTGGG 907
Db 810 TCTTCAAGCTGTACTGAGCATAGGCTGGGAGTTCGGCTGTCTGTTATCCCTGGG 869
QY 908 CAAATGGGAAGCTGTACTAGCAAAATAGAAAGTGTGTTTGGCAAAAGCCCTGGGGGT 967
Db 870 GCATGTGCAAGTATCTTACGAGGACGAGGGTGTCTG---ACCAGGAATCTCAACATGA 926
QY 968 ACACCGACTACATCTACAGGGCCCATGATCTGCTGCTGCTGATCAATTTCTCTCC 1027
Db 927 ACTATTGGCTCATACATACGCTTGGCCATCTCTTTGCAATCGGGGTCAACTTCTTGTCT 986
QY 1028 TTTTCAACATCTGCGCATCTCATGACCAAGCTTCGGGGATCCACCATCTCGAGACCA 1087
Db 987 TCATCCGGGTCACTGATGCTGATGACCAAGCTGAAGGCTATCTCATGTGTAGACCG 1046
QY 1088 TTCAGTACAGGAAGCTGTGAAAGCACTCTGTGTGCTGTGCTGCTGCTGCTGCTGCT 1147
Db 1047 ACATCAAAATGCAGACTCGCAAGTCCACTCTGAGCTCATCCGCTTCTGGGCAAGCATG 1106
QY 1148 ACATGCTGTTCTTGGTCAATCCCGGGGAGG-----TGAGGTCTCCGGGTCTCTTCA 1201
Db 1107 AAGTCATCTTTTGGCTTGTGATGAGCAGACGCCCGGAGGAACTTACGCTTCTGTCAAGC 1166
QY 1202 TCTACTTCAACTCTTCTGGAATCTTCCAGGGCTTCTTTGTGTCTGTCTTCTACTGTT 1261

Db 1167 TGTTACAGAGCTCTCTTCACTTCTTCCAGGGCTTATGTGGCTGTCTTGTACTGCT 1226
QY 1262 TCTCTAATAGTAGGTCCGTTCTTCCATCCGGAAGAGTGGACCGGTGGCAGGACAAGC 1321
Db 1227 TTGTCAACAATGAGTCCAGATGGAGTTTTCGGAAGAGCTGGGAGCGCTGGAGCTGGAGC 1286
QY 1322 ACTCGATCCGTCGCCAGTGGCGGTCATGTCCATCCCACTCCCAACCCCGGTGCA 1381
Db 1287 GCTTGAACATCCAGAGGGACAGCAGCATGAAACCCCTCAAGTGTCTCCACAGCAGGTCA 1346
QY 1382 GC 1383
Db 1347 GC 1348

RESULT 9

US-11-136-527-1893
; Sequence 1893, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1893
; LENGTH: 3453
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-1893

Query Match 8.1%; Score 128.4; DB 12; Length 3453;
Best Local Similarity 52.8%; Pred. No. 1.7e-22;
Matches 323; Conservative 2; Mismatches 278; Indels 9; Gaps 2;
QY 709 CACAGAGCAACGTGGGCTGTGCGAGTTGGTGACAGCGCGCTTACAACTACTTCCATGTG 768
Db 988 CATGACAGTGAAGTGAATGCAAGTTGCAAGTCTGCACTTTTCCATCAGTACATGATGGCT 1047
QY 769 ACCAATCTTCTGAGTGTTCGGCAGGGCTGTCTGCTACACACAGCCATCGTGTCTACC 828
Db 1048 TGCAACTACTTCTGGATGCTGTGTGAGGGGATCTATCTTCACTCTGATCGTATGGCT 1107
QY 829 TACTCCACTGACCGGTGGCAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 888
Db 1108 GTGTTACAGAGATCAAGCTGTGCGCTGTACTATTTACTTGGCTGGGGTTCCCAATA 1167
QY 889 CCCATCAATGTGGCTGGGCCATTTGGGAAGCTGTACTACGACAAATGAGAAGTGTCTGTTT 948
Db 1168 GTGCCAACTATTATCCATGCCATTTACTGTCGGCTCTATACAAAGCAACTGTTGGCT- 1226
QY 949 GGCAGAAAGCCCTGGGGTGTACACCGACTACCTACCGGGGCCCATGATCTGTGTCTGTG 1008
Db 1227 -----GAGTACGAGAGACCCCATTTGCTTTTACATCATCCATGAGACCCGCTCATGGCGGCTCTG 1281
QY 1009 CTGATCAATTTTCATCTTCTTTTCAACATCTGTCGCGCATCTCATGACCAAGCTCCCGGCA 1068
Db 1282 GTGGTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1341
QY 1069 TCCACCACTCTGAGACCACTTTCAGTACAGGAAGGCTGTGAAAGGCCACTCTGTGTGTGCTG 1128
Db 1342 ACCATGAAGCCGAGGCTTACATGATGATGATGATGATGATGATGATGATGATGATGATG 1401
QY 1129 CCGCTCTCGGGATCACTTACATGCTGTCTTCTGTCATATCCCGGGGAGGATGAGGTCTCC 1188
Db 1402 CCGCTGCTGGGATCAGT 1458

QY 1189 CGGGTGGTCTTCTATCTACTTCAACTCTTCTCGAATCCTTCCAGGCTCTTTGTGTCT 1248
Db 1459 GGAAGATCTATGATATCTCATGCACTCTCTGATTCATTTCCAGGATCTTTGTGGCG 1518
QY 1249 GTGTTCTACTGTTTCTCTCAATAGTAGGTCGGTTCTCCATCCGGAAGAGGTGGCACCGG 1308
Db 1519 ACTATCTACTGTTCTCTTACCATGAGTGAAGTGACCTTGAAGCGTCAAGTGGGCGCAG 1578

QY 1309 TGGCAGGACAAAG 1320

Db 1579 TTCAAGATCCAG 1590

RESULT 10

US-11-136-527-1894
; Sequence 1894, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AMI01086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1894
; LENGTH: 3434
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-1894

Query/Match 7.9%; Score 124.6; DB 12; Length 3434;

Best Local Similarity 53.1%; Pred. No. 1.5e-21; Indels 9; Gaps 2;
Matches 315; Conservative 0; Mismatches 269;

QY 728 GGTGAGGTTGGTGACAGCGCCCTACAACTACTTCCATGTGACCAACTTCTCTGGATGT 787
Db 949 GTTGCAAGATCTTGCATCTTTTCCATCAGTACATGATGGCTTCACTACTCTTGGATGC 1008
QY 788 TCGCGAGGCTGCTACCTGCACAGCCATCTGTCTCACTACTCACTGACGGGTGC 847
Db 1009 TGTGTGAGGGGATCTATCTTCACTCTGATCGTCACTGGCTGTGTTCCACGAGGATCAAC 1068
QY 848 GCAAAATGATGTTCACTGCAATGGCTGGGGTGTGCCCTTCCCATCATTTGCGCCCTGG 907
Db 1069 GTCTGGCTGGTACTATTTACTTGGCTGGGGGTTCCTCAATAGTGCCAACTATTATCAATG 1128
QY 908 CCATTGGGAAGCTGTACTACGACAAATGAGAAGTGTCTGTTTGGCAAAAGGCTGGGGTGT 967
Db 1129 CCATTACTCGTGGCTTACTACACGACAACTGTGGCTGAGTA-----CGGAGACCC 1182
QY 968 ACACGACTACATCTACCGAGGCCCCATGATCTGTGCTGTGATCAATTTCACTTCC 1027
Db 1183 ACTTGTCTTACATCATCCATGAGCCCCGTATGCGGGCTCTGGTGGTCAACTTCTTCTTTC 1242
QY 1028 TTTTCAACATCGTCCGATCCTCATGACCAAGCTCCGGGATCCACACGCTCTGAGACCA 1087
Db 1243 TGCTCAACATGTGCGGTGCTGTGTGACCAAGATGAGGCAAAACCATGAGCCGAGGCT 1302
QY 1088 TTCAGTACAGAAAGGCTGTGAAGACCACTCTGTGTGCTGTGCTGCCCTCTGGGATCACCT 1147
Db 1303 ACATGTACCTGAAGGCTGTAAAGCCACCATGTTCTGTGCCCCCTGCTGGGATCCAGT 1362
QY 1148 ACATGCTGTTCTTGTCAATCCCGGGAGAGATGAGGTCTCCCGGGTGTCTTCACTTACT 1207
Db 1363 TTGTGTGTTTCTCTGAGGCCCCCTCCAAAGAGTGTCT---TGGGAAGATCTATGATATC 1419
QY 1208 TCAACTCTCTCTGGATCTCTTCAGGGCTCTTGTGTGCTGTGTCTTACTGTTCTCTCA 1267
Db 1420 TCATGCACTCTCTGATTTTCAGGGATTTCTTGTGCGGACTATCTACTGCTTCTGTA 1479

QY 1268 ATAGTCAGGTCCGTTCTTCCATCCGGAAGAGGTGGCACCGGTGGCAGGACAAG 1320
Db 1480 ACCATGAGGTGCAAGTAGACCTTGAAGCGTCAGTGGCGCAGTTCAAGATCCAG 1532

RESULT 11

US-09-925-065A-506766/c
; Sequence 506766, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 506766
; LENGTH: 613
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-506766

Query/Match 7.8%; Score 124; DB 6; Length 613;

Best Local Similarity 100.0%; Pred. No. 1.5e-21; Indels 0; Gaps 0;
Matches 124; Conservative 0; Mismatches 0;

QY 601 AGGAGCATCCGTCCTGGGAAACATCATCCACTGGAACCTCATCTCCGCTTTCATCCTG 660
Db 356 AGGAGCATCCGTCCTGGGAAACATCATCCACTGGAACCTCATCTCCGCTTTCATCCTG 297
QY 661 CGCAAGCCACCTGTCGTGTGTCAGCTAACCATGAGCCCCGAGGTCCACCAAGAGCAAC 720
Db 296 CGCAAGCCACCTGTCGTGTGTCAGCTAACCATGAGCCCCGAGGTCCACCAAGAGCAAC 237
QY 721 GTGG 724
Db 236 GTGG 233

RESULT 12

US-11-136-527-4065
; Sequence 4065, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AMI01086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4065
; LENGTH: 1806
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-4065


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; NAME/KEY: misc feature
; LOCATION: (1560)..(1607)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2217)..(2276)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2561)..(2580)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-870

Query Match      6.2%; Score 98; DB 12; Length 2786;
Best Local Similarity 51.1%; Pred. No. 7.3e-15;
Matches 286; Conservative 0; Mismatches 265; Indels 9; Gaps 2;

QY 753 CAACTACTTCCATGTGACCAACTTCTTCTGGATGTTTCGGCGAGGGCTGTACCTGCACAC 812
DB 819 CCAGTACTCGTGGTGCCCACTTACACTTGGCTGCTGGTAGAGGGTGTATACCTGCACCA 878
QY 813 AGCCATCGTCTCACCTACTCCACTGACCGGCTGCGCAAAATGGATGTTCACTGCAATTGG 872
DB 879 TCTGCTGGTGATCGTGGAGGCTCGGAAAGGCCACTTCCGCTGTACTCTGCTTCTGG 938
QY 873 CTGGGGTGGCCCTTCCCATCATCTTCCCATCATCTTGGCTGGCCATTTGGGAAGCTGTGACCAA 932
DB 939 CTGGGGGGCCCCCGCGCTTTTCGTCTCATCTTCTGGGTGATCGTCAGGTACCTGCTGGAGAA 998
QY 933 TGAGAAAGTGTGTTTGGCAAAAGGCGCTGGGGTGTATACCGACTACATCTTACAGGCCCC 992
DB 999 CACGAGTGTCTGGAGCGGCAACCGAGGTCAAAGC---CATTTGGTGGATCATTCGACCCCC 1055
QY 993 CATGATCTCTGGTCTGCTGATCAATTTTCATCTTCTTTTCAACATCGTCGCGATCCTCAT 1052
DB 1056 CATCTTAATAACCATCTTGTATCAATTTCTCATCTTCCATCCGCATCTTGGCATCTTGT 1115
QY 1053 GACCAAGCTCCGGGCATCCACCGTCTGAGACCATTCAGTACAGGAAGCTGTGAAAGC 1112
DB 1116 GTCAAAACTCAGGACCGGCGAGATGCGTCCCGGACTACCGACTGCGGCTGCTGCTTC 1175
QY 1113 CACTCTGGTCTGCTGCCCTCTGGGCATCACTACATCTGTTCTTCCTCAATCCCGG 1172
DB 1176 CACGCTGACGCTGGTGCCCTCTGCTGGGTGTCACAGGGTGGTGTGGCCCGCGTACGGA 1235
QY 1173 GGA-----GGATGAGGTCTCCCGGGTGGTCTTTCATCTACTTCAACTCTTCTTGGAAATC 1226
DB 1236 GGAACAGGCTGAAAGGCACCTCGCGCTTGGCAAACTGGCCCTTCGAATCTTCTTAAGTTC 1295
QY 1227 CTTCCAGGGCTTCTTGTGCTGTCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 1286
DB 1296 CTTCCAGGGATTTCTGCTGAGCGTGTCTACTGCTTTCATCAACAAGAGGTGCAGTCCGA 1355
QY 1287 CATCCGGAAGAGGTGGCACC 1306
DB 1356 GATCCGCGGAGCTGGCGCC 1375
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RESULT 15
US-11-128-049-870
; Sequence 870, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; MAKING AND USING SAME
```

```
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 870
; LENGTH: 2786
; TYPE: DNA
; ORGANISM: Cricetulus sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (132)..(151)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1560)..(1607)
; OTHER INFORMATION: n is a, c, g, or t
; NAME/KEY: misc feature
; LOCATION: (2217)..(2276)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2561)..(2580)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-049-870
```

```
Query Match      6.2%; Score 98; DB 12; Length 2786;
Best Local Similarity 51.1%; Pred. No. 7.3e-15;
Matches 286; Conservative 0; Mismatches 265; Indels 9; Gaps 2;

QY 753 CAACTACTTCCATGTGACCAACTTCTTCTGGATGTTTCGGCGAGGGCTGTACCTGCACAC 812
DB 819 CCAGTACTCGTGGTGCCCACTTACACTTGGCTGCTGGTAGAGGGTGTATACCTGCACCA 878
QY 813 AGCCATCGTCTCACCTACTCCACTGACCGGCTGCGCAAAATGGATGTTCACTGCAATTGG 872
DB 879 TCTGCTGGTGATCGTGGAGGCTCGGAAAGGCCACTTCCGCTGTACTCTGCTTCTGG 938
QY 873 CTGGGGTGGCCCTTCCCATCATCTTCCCATCATCTTGGCTGGCCATTTGGGAAGCTGTGACCAA 932
DB 939 CTGGGGGGCCCCCGCGCTTTTCGTCTCATCTTCTGGGTGATCGTCAGGTACCTGCTGGAGAA 998
QY 933 TGAGAAAGTGTGTTTGGCAAAAGGCGCTGGGGTGTATACCGACTACATCTTACAGGCCCC 992
DB 999 CACGAGTGTCTGGAGCGGCAACCGAGGTCAAAGC---CATTTGGTGGATCATTCGACCCCC 1055
QY 993 CATGATCTCTGGTCTGCTGATCAATTTTCATCTTCTTTTCAACATCGTCGCGATCCTCAT 1052
DB 1056 CATCTTAATAACCATCTTGTATCAATTTCTCATCTTCCATCCGCATCTTGGCATCTTGT 1115
QY 1053 GACCAAGCTCCGGGCATCCACCGTCTGAGACCATTCAGTACAGGAAGCTGTGAAAGC 1112
DB 1116 GTCAAAACTCAGGACCGGCGAGATGCGTCCCGGACTACCGACTGCGGCTGCTGCTTC 1175
QY 1113 CACTCTGGTCTGCTGCCCTCTGGGCATCACTACATCTGTTCTTCCTCAATCCCGG 1172
DB 1176 CACGCTGACGCTGGTGCCCTCTGCTGGGTGTCACAGGGTGGTGTGGCCCGCGTACGGA 1235
QY 1173 GGA-----GGATGAGGTCTCCCGGGTGGTCTTTCATCTACTTCAACTCTTCTTGGAAATC 1226
DB 1236 GGAACAGGCTGAAAGGCACCTCGCGCTTGGCAAACTGGCCCTTCGAATCTTCTTAAGTTC 1295
QY 1227 CTTCCAGGGCTTCTTGTGCTGTCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 1286
DB 1296 CTTCCAGGGATTTCTGCTGAGCGTGTCTACTGCTTTCATCAACAAGAGGTGCAGTCCGA 1355
QY 1287 CATCCGGAAGAGGTGGCACC 1306
DB 1356 GATCCGCGGAGCTGGCGCC 1375
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Search completed: March 17, 2006, 11:08:49
Job time : 583 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 16, 2006, 17:12:55 ; Search time 192 Seconds
(without alignments)
1016.063 Million cell updates/sec

Title: US-10-649-193-15
Perfect score: 2381
Sequence: 1 MGHQPQLRVKALLLGLNP.....SIPTSPTRVSFHSIKQSTAV 444

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2381	100.0	444	4	AAB71866 Human CRF
2	2381	100.0	444	5	AAB71866 Human CRF
3	2381	100.0	444	6	ABR43052 Human CRH
4	2381	100.0	444	6	ABU08081 Human cor
5	2381	100.0	444	6	ABG76402 Human hCR
6	2381	100.0	444	7	ADJ65810 Human cor
7	2381	100.0	444	8	ADJ65810 Human cor
8	2324	97.6	447	7	ADJ65810 Human cor
9	2186.5	91.8	415	2	AAR97290 Human CRF
10	2186.5	91.8	415	2	AAR97290 Human CRF
11	2186.5	91.8	415	2	AAR97290 Human CRF
12	2186.5	91.8	415	5	AAR97290 Human CRF
13	2186.5	91.8	415	5	AAR97290 Human CRF
14	2186.5	91.8	415	5	AAR97290 Human CRF
15	2186.5	91.8	415	5	AAR97290 Human CRF
16	2186.5	91.8	415	5	AAR97290 Human CRF
17	2186.5	91.8	415	6	ABU08075 Human cor
18	2186.5	91.8	415	6	ABG76046 Human cor
19	2186.5	91.8	415	8	ADJ65797 Human cor
20	2186.5	91.8	415	8	ADJ65797 Human cor
21	2186.5	91.8	415	8	ADJ65797 Human cor
22	2186.5	91.8	415	8	ADJ65797 Human cor
23	2180.5	91.6	415	4	ABR43051 Human CRH
24	2137.5	89.8	415	2	AAR97294 Mouse CRF

25	2137.5	89.8	415	5	AAE26684	Aae26684 Mouse CRF
26	2137.5	89.8	415	5	AAO19430	Aao19430 Murine CO
27	2137.5	89.8	415	6	ABR43059	AbR43059 Mouse CRH
28	2137.5	89.8	415	6	ABU08080	Abu08080 Mouse cor
29	2137.5	89.8	415	6	ABG76401	Abg76401 Mouse cor
30	2137.5	89.8	415	8	ADJ65808	Adj65808 Mouse cor
31	2137.5	89.8	415	8	ADJ65808	Adj65808 Mouse cor
32	2137.5	89.8	415	8	ADJ65808	Adj65808 Mouse cor
33	2126.5	89.3	415	2	AAR97292	Aar97292 Rat CRF I
34	2126.5	89.3	415	2	AAR97292	Aar97292 Rat CRF I
35	2126.5	89.3	415	2	ABU62361	Abu62361 Rat corti
36	2126.5	89.3	415	5	AAE26681	Aae26681 Rat CRF-R
37	2126.5	89.3	415	5	AAO19427	Aao19427 Rat corti
38	2126.5	89.3	415	5	AAO19439	Aao19439 Bovine CO
39	2126.5	89.3	415	6	ABU08077	Abu08077 Rat corti
40	2126.5	89.3	415	6	ABG76048	Abg76048 Rat corti
41	2126.5	89.3	415	7	ADJ65801	Adj65801 Rat Prote
42	2126.5	89.3	415	8	ADJ65801	Adj65801 Rat corti
43	2126.5	89.3	415	8	ADJ65801	Adj65801 Rat corti
44	2126.5	89.3	415	8	ADJ65801	Adj65801 Rat corti
45	2092.5	87.9	401	5	AAU96998	Aau96998 Human CRH

ALIGNMENTS

RESULT 1

AAB71866

ID AAB71866 standard; protein; 444 AA.

XX

AC AAB71866;

XX

DT 03-MAY-2001 (first entry)

XX

DE Human CRP1 seven transmembrane domain.

XX

KW Human; CRP1; corticotropin releasing factor receptor 1; h15571;

KW immunomodulatory; vascular; hepatic; antiasthma; antimicrobial;

KW antiinflammatory; immunosuppressive; gene therapy; vaccine;

KW G-protein coupled receptor; GPCR; liver fibrosis; respiratory disorder;

KW infection; chronic inflammatory disease; organ-specific autoimmunity;

KW graft rejection; cystic fibrosis.

XX

OS Homo sapiens.

XX

PN WO200109328-A1.

XX

PD 08-FEB-2001.

XX

PF 03-AUG-2000; 2000WO-US021278.

XX

XX Aae26685 Human CRF

PR ABR43052 Human CRH

PR ABU08081 Human cor

PR ABG76402 Human hCR

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX

PI Hodge MR, Lloyd C, Welch NS;

XX

DR WPI; 2001-138653/14.

XX

PT Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful

PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma.

PS

PS Disclosure; Fig 2; 145pp; English.

XX

CC The present sequence is a human G-protein coupled receptor (GPCR) used

CC for comparison with the seven transmembrane domain of a novel GPCR

CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be

CC used in the prevention, treatment and diagnosis of diseases associated

CC with inappropriate GPCR expression. Such diseases include immune,

CC haematological, fibrotic, hepatic and respiratory disorders including

CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic

CC infections, chronic inflammatory diseases, organ-specific autoimmunity,

CC graft rejection, graft versus host disease, cystic fibrosis and, in
 CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens
 CC in the production of antibodies against GPCR and in assays to identify
 CC modulators (agonists and antagonists) of GPCR expression and activity.
 CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
 CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
 CC used as diagnostic agents for detecting the presence of GPCR polypeptides
 CC in samples

XX Sequence 444 AA;

Query Match 100.0%; Score 2381; DB 4; Length 444;
 Best Local Similarity 100.0%; Pred. No. 8.9e-245;
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGHPQLRVKALLLLGLNPNVSLQDQCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
 DB 1 MGGHPQLRVKALLLLGLNPNVSLQDQCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
 QY 61 GOLVVRPCPAFFVGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKKSKVHVAV 120
 DB 61 GOLVVRPCPAFFVGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKKSKVHVAV 120
 QY 121 IINYLGHCSILVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPQVRSIRCLR 180
 DB 121 IINYLGHCSILVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPQVRSIRCLR 180
 QY 181 NIIHWNLSAFILRNATWVQLTMSPEVHQSNVGCRLVTAAYNYFHTNPFWMFEGGC 240
 DB 181 NIIHWNLSAFILRNATWVQLTMSPEVHQSNVGCRLVTAAYNYFHTNPFWMFEGGC 240
 QY 241 YLHTAIVLTYSTDLRKWMFICIGWGPFPPIIVAWAIGKLYYDNEKCFGRPGVTDYI 300
 DB 241 YLHTAIVLTYSTDLRKWMFICIGWGPFPPIIVAWAIGKLYYDNEKCFGRPGVTDYI 300
 QY 301 YQGPMLVLLINFIPLFNIVRLMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF 360
 DB 301 YQGPMLVLLINFIPLFNIVRLMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF 360
 QY 361 VNPGEDEVSRVVIYFNFSFLESFQGFVSVFYCFLNSEVRSAIRKRWHRQDKHSIRARV 420
 DB 361 VNPGEDEVSRVVIYFNFSFLESFQGFVSVFYCFLNSEVRSAIRKRWHRQDKHSIRARV 420
 QY 421 ARAMSIPTSPTRVSPHSIKOSTAV 444
 DB 421 ARAMSIPTSPTRVSPHSIKOSTAV 444

RESULT 2

ID AAE26685 standard; protein; 444 AA.

XX AAE26685;

AC AAE26685;

XX 13-DEC-2002 (first entry)

DE Human CRF-RA2 splice variant protein.

XX Human, G protein-coupled corticotropin-releasing factor receptor; CRF;

XX CRF-R; adrenocorticotrophic hormone; irritable bowel syndrome; therapy;

XX Cushing's syndrome; pituitary tumour; chronic stress; anorexia nervosa;

XX receptor; alcoholism; CRF-RA2.

XX Homo sapiens.

OS US2002055617-A1.

XX 09-MAY-2002.

XX 12-NOV-1998; 98US-00191724.

XX 18-JUN-1993; 93US-00079320.

XX 23-AUG-1993; 93US-00110286.

PR

PR 25-MAY-1994; 94WO-US005908.
 PR 09-DEC-1994; 94US-00353537.
 PR 07-JUN-1995; 95US-00483139.
 XX (PERR/) PERRIN M H.
 PA (CHEN/) CHEN R.
 PA (LEW/) LEWIS K A.
 PA (VALE/) VALE W W.
 PA (DONA/) DONALDSON C J.
 PA (SAWC/) SAWCHENKO P.
 XX
 PI Perrin MH, Chen R, Lewis KA, Vale WM, Donaldson CJ, Sawchenko P;
 DR WPI: 2002-462916/49.
 DR N-PSDB; AAD44489.
 XX
 PT New isolated recombinant mammalian G protein-coupled corticotropin-
 PT releasing factor receptor protein for treating e.g. Cushing's syndrome,
 PT pituitary tumors, stress, anorexia, alcoholism or irritable bowel
 PT syndrome.
 XX
 PS Claim 9; Page 33-34; 44pp; English.
 XX
 CC The invention relates to recombinant mammalian G protein-coupled
 CC corticotropin-releasing factor (CRF) receptor (CRF-R) proteins having
 CC high affinity for CRF and nucleic acid molecules encoding such receptor
 CC proteins. Polypeptides of the invention can be used to reduce high levels
 CC of adrenocorticotrophic hormone caused by excess CRF and so can be used
 CC to treat diseases such as Cushing's syndrome, pituitary tumours, chronic
 CC stress, anorexia nervosa, alcoholism and irritable bowel syndrome. They
 CC are used in pharmaceuticals and in the production of antibodies. The
 CC present sequence is human CRF-RA2 splice variant protein
 XX
 SQ Sequence 444 AA;

Query Match 100.0%; Score 2381; DB 5; Length 444;
 Best Local Similarity 100.0%; Pred. No. 8.9e-245;
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGHPQLRVKALLLLGLNPNVSLQDQCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
 DB 1 MGGHPQLRVKALLLLGLNPNVSLQDQCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
 QY 61 GOLVVRPCPAFFVGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKKSKVHVAV 120
 DB 61 GOLVVRPCPAFFVGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKKSKVHVAV 120
 QY 121 IINYLGHCSILVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPQVRSIRCLR 180
 DB 121 IINYLGHCSILVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPQVRSIRCLR 180
 QY 181 NIIHWNLSAFILRNATWVQLTMSPEVHQSNVGCRLVTAAYNYFHTNPFWMFEGGC 240
 DB 181 NIIHWNLSAFILRNATWVQLTMSPEVHQSNVGCRLVTAAYNYFHTNPFWMFEGGC 240
 QY 241 YLHTAIVLTYSTDLRKWMFICIGWGPFPPIIVAWAIGKLYYDNEKCFGRPGVTDYI 300
 DB 241 YLHTAIVLTYSTDLRKWMFICIGWGPFPPIIVAWAIGKLYYDNEKCFGRPGVTDYI 300
 QY 301 YQGPMLVLLINFIPLFNIVRLMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF 360
 DB 301 YQGPMLVLLINFIPLFNIVRLMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF 360
 QY 361 VNPGEDEVSRVVIYFNFSFLESFQGFVSVFYCFLNSEVRSAIRKRWHRQDKHSIRARV 420
 DB 361 VNPGEDEVSRVVIYFNFSFLESFQGFVSVFYCFLNSEVRSAIRKRWHRQDKHSIRARV 420
 QY 421 ARAMSIPTSPTRVSPHSIKOSTAV 444
 DB 421 ARAMSIPTSPTRVSPHSIKOSTAV 444

RESULT 3

ABR43052
 ID ABR43052 standard; protein; 444 AA.
 XX
 AC ABR43052;
 XX
 DT 03-JUL-2003 (first entry)
 XX
 DE Human CRH-R1 beta protein SEQ ID NO:2.
 XX
 KW Human; corticotropin releasing hormone receptor type 1; CRH-R1;
 KW antipsoriatic; antiallergic; immunosuppressive; antiinflammatory;
 KW dermatological; pathophysiological state; neuroendocrine disorder;
 KW hyperproliferative epidermal disorder; allergic contact dermatitis;
 KW autoimmune disorder; epidermal carcinogenesis; malignant transformation;
 KW epidermal melanocyte; dermal melanocyte; chromosome 17.
 XX
 OS Homo sapiens.
 XX
 PN WO2003024990-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 13-SEP-2002; 2002WO-US029117.
 XX
 PR 14-SEP-2001; 2001US-0322195P.
 XX
 PA (UYTE-) UNIV TENNESSEE RES CORP.
 XX
 PI Pisarchik A, Slominski A;
 XX
 DR WPI; 2003-313342/30.
 XX
 PT Novel DNA encoding corticotropin releasing hormone receptor type 1 which
 PT is useful for treating pathophysiological state such as inflammatory skin
 PT disease e.g. psoriasis and allergic contact dermatitis.
 XX
 PS Example 5; Fig 5A-C; 110pp; English.
 XX
 CC The present invention describes DNA (I) encoding a corticotropin
 CC releasing hormone receptor type 1 (CRH-R1) protein comprising an amino
 CC acid sequence given in ABR43055 to ABR43071. Also describe: (1) a vector
 CC (II) capable of expressing (I) or its degenerate variant, and comprising
 CC (1) or its degenerate variant, and regulatory elements necessary for
 CC expression of the DNA in a cell; (2) a host cell (III) transfected with
 CC (II); (3) an isolated CRH-R1 protein (IV) encoded by (1); (4) an antibody
 CC (V) directed against (IV); (5) a pharmaceutical composition (VI)
 CC comprising (IV), and a carrier; and (6) protecting (M) skin cells against
 CC damage induced by an environmental factor, by inducing the expression of
 CC CRH-R type Ig in the skin cells, where the expression of the receptor
 CC protects the skin cells against the damage. CRH-R1 has antipsoriatic,
 CC antiallergic, immunosuppressive, antiinflammatory and dermatological
 CC activities. (VI) can be used for treating a pathophysiological state such
 CC as hyperproliferative epidermal disorder, neuroendocrine disorder,
 CC allergic contact dermatitis, autoimmune disorder, epidermal
 CC carcinogenesis, malignant transformation of epidermal or dermal
 CC melanocytes. (M) is useful for protecting (M) skin cells against damage
 CC induced by an environmental factor such as solar radiation. Human CRH-R1
 CC is located on chromosome 17, and mouse CRH-R1 is located to chromosome
 CC 11. The present sequence represents human CRH-R1 beta (see Genbank
 CC accession number U23333), which is used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 444 AA;
 XX

Query Match 100.0%; Score 2381; DB 6; Length 444;
 Best Local Similarity 100.0%; Pred. No. 8.9e-245;
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX

QY 1 MGGHPQLRLVKALLLGLNVPVSLQDOHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
 DB 1 MGGHPQLRLVKALLLGLNVPVSLQDOHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
 QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARNVYSECOEILNEEKSKVHYHAV 120

Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARNVYSECOEILNEEKSKVHYHAV 120
 QY 121 IINYLGHGISLVALLVAFVLFLRLRPGCTHWGDAQDGALEVGAPWSGAPQVRSIRCLR 180
 Db 121 IINYLGHGISLVALLVAFVLFLRLRPGCTHWGDAQDGALEVGAPWSGAPQVRSIRCLR 180
 QY 181 NIIHWNLI SAFILRNATFWVQLTMSPEVHQSNVGCRLVTAAYNYFHVTFNPFMFGECC 240
 Db 181 NIIHWNLI SAFILRNATFWVQLTMSPEVHQSNVGCRLVTAAYNYFHVTFNPFMFGECC 240
 QY 241 YLHTALVLYSTYDRLRKMMFICIGWGVPPPII VAWAIGKLYYDNEKWCWFGKRGVYTDYI 300
 Db 241 YLHTALVLYSTYDRLRKMMFICIGWGVPPPII VAWAIGKLYYDNEKWCWFGKRGVYTDYI 300
 QY 301 YQGPMLVLLINFIPLFNIVRIIMTKLRASVTTSETIOYRKAVKATILVLLPLLGITYMLFF 360
 Db 301 YQGPMLVLLINFIPLFNIVRIIMTKLRASVTTSETIOYRKAVKATILVLLPLLGITYMLFF 360
 QY 361 VNPGEDEVSRVPIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
 Db 361 VNPGEDEVSRVPIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
 QY 421 ARAMSIPTSPTRVSPHSIKOSTAV 444
 Db 421 ARAMSIPTSPTRVSPHSIKOSTAV 444

RESULT 4
 ABU08081
 ID ABU08081 standard; protein; 444 AA.
 XX
 AC ABU08081;
 XX
 DT 21-MAY-2003 (first entry)
 XX
 DE Human corticotropin-releasing factor receptor 2 (CRF-R2).
 XX
 KW Human; receptor; corticotropin-releasing factor receptor; CRF;
 KW G protein-coupled corticotropin-releasing factor receptor;
 KW hypothalamic peptide; pituitary adrenocorticotrophic hormone; ACTH;
 KW adrenal glucocorticoid; gene therapy; cortisol; Alzheimer's disease;
 KW Cushing's disease; anorexia nervosa; alcoholism; antiinflammatory;
 KW irritable bowel syndrome; melancholic depression; neuroprotective;
 KW nootropic; antidepressant; splice variant.
 XX
 OS Homo sapiens.
 XX
 PN US6495343-B1.
 XX
 PD 17-DEC-2002.
 XX
 PF 17-JAN-1995; 95US-00374009.
 XX
 PR 18-JUN-1993; 93US-00079320.
 PR 23-AUG-1993; 93US-00110286.
 PR 25-MAY-1994; 94WO-US005908.
 PR 09-DEC-1994; 94US-00353537.
 XX
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Perrin MH, Chen R, Lewis KA, Vale WW, Donaldson CJ, Sawchenko P;
 XX
 DR WPI; 2003-327461/31.
 XX
 DR N-PSDB; ABX93041.
 XX
 PT New nucleic acid and its encoded G protein-coupled corticotropin-
 PT releasing factor receptor, useful for diagnosing or treating e.g. ACTH
 PT levels or high cortisol levels associated with Alzheimer's disease or
 PT Cushing's disease.
 XX
 PS Disclosure; Col 61-64; 42pp; English.
 XX

CC The invention discloses an isolated nucleic acid, which encodes a
CC mammalian G protein-coupled corticotropin-releasing factor (CRF) receptor
CC protein. CRF is a hypothalamic peptide which stimulates the secretion and
CC biosynthesis of pituitary adrenocorticotrophic hormone (ACTH) leading to
CC increased adrenal glucocorticoid production. The nucleic acid, or the CRF
CC receptor that it encodes, is useful in bioassays. The nucleic acid, or the CRF
CC receptor is particularly useful for providing recombinant receptors that
CC allows the development of less expensive, more sensitive and automated
CC means for assaying CRF and CRF-like compounds and developing CRF-based
CC therapeutics. The nucleic acid, or fragments of its encoded receptor, are
CC useful in therapy, e.g. gene therapy for reducing ACTH levels or treating
CC high cortisol levels associated with Alzheimer's diseases, Cushing's
CC diseases, anorexia nervosa, alcoholism or irritable bowel syndrome. These
CC are also useful in diagnostic assays, e.g. for diagnosing Alzheimer's
CC diseases, melancholic depression, anorexia nervosa, Cushing's diseases or
CC alcoholism. The sequence presented is the human splice variant of CRF-R1,
CC CRF-R2, protein
XX
SQ Sequence 444 AA;

Query Match 100.0%; Score 2381; DB 6; Length 444;
Best Local Similarity 100.0%; Pred. No. 8.9e-245;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGHPQLRLVKALLLGLNPVSASLQDQCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
Db 1 MGGHPQLRLVKALLLGLNPVSASLQDQCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GOLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECOEILNEEKSKVHHVAV 120
Db 61 GOLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECOEILNEEKSKVHHVAV 120
QY 121 IINYLGHCSLVALLVAFVLFLRLPGCTHWGDAQDGALEVGAPWGSAPPQVRSIRCLR 180
Db 121 IINYLGHCSLVALLVAFVLFLRLPGCTHWGDAQDGALEVGAPWGSAPPQVRSIRCLR 180
QY 181 NIIHWNLSAFILRNATFVVQLTMSPEVHQSNVGCRLVTAAYNFHVTFNPFMFGECC 240
Db 181 NIIHWNLSAFILRNATFVVQLTMSPEVHQSNVGCRLVTAAYNFHVTFNPFMFGECC 240
QY 241 YLHTAIVLYTSDRLRKWPCICIGWGPPIIVAMAIGKLYDNEKWCGRKRGVYTDYI 300
Db 241 YLHTAIVLYTSDRLRKWPCICIGWGPPIIVAMAIGKLYDNEKWCGRKRGVYTDYI 300
QY 301 YQGPMLVLLINFIPLFNVIILMTKLRASTTSETIQYRKAVKATVLLPLLGITVWLFF 360
Db 301 YQGPMLVLLINFIPLFNVIILMTKLRASTTSETIQYRKAVKATVLLPLLGITVWLFF 360
QY 361 VNPGEDEVSRVFIYFNSFLESFQGFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 420
Db 361 VNPGEDEVSRVFIYFNSFLESFQGFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 420
QY 421 ARAMSIPTSPTRVSHSIKQSTAV 444
Db 421 ARAMSIPTSPTRVSHSIKQSTAV 444

RESULT 5
ABG76402
ID ABG76402 standard; protein; 444 AA.
XX
AC ABG76402;
XX
DT 07-MAY-2003 (first entry)
XX
DE Human hCRF-RAL, splice variant.
XX
KW Human; receptor; corticotropin releasing factor receptor; hCRF-RAL;
KW Cushing's disease; pituitary tumour; Alzheimer's disease;
KW melancholic depression; anorexia nervosa; chronic stress; alcoholism;
KW hypercortisolemia; gastrointestinal disorder; irritable bowel syndrome;
KW pre-eclampsia; pregnancy-induced complication; arthritis; abortion;
KW twinning.

XX Homo sapiens.
OS US6482608-B1.
PN 19-NOV-2002.
XX 26-MAY-2000; 2000US-00580734.
XX 18-JUN-1993; 93US-00079320.
PR 23-AUG-1993; 93US-00110286.
PR 25-MAY-1994; 94WO-US0005908.
PR 09-DEC-1994; 94US-00353537.
PR 17-JAN-1995; 95US-00374009.
PR 07-JUN-1995; 95US-00483139.
PR 12-NOV-1998; 98US-00191724.
XX (SALK) SALK INST BIOLOGICAL STUDIES.
XX Perrin MH, Chen R, Lewis KA, Vale WW, Donaldson CJ, Sawchenko P;
PI WPI: 2003-287359/28.
XX N-PSDB; ABX11840.
PT Novel cell line expressing nucleic acid expression vector comprising
PT nucleic acid encoding human corticotropin releasing factor (CRF) receptor
PT useful for reducing high adrenocorticotropin hormone, by binding to CRF.
XX Disclosure; Col 61-64; 42pp; English.
PS The invention relates to a cell line expressing a recombinant
CC corticotropin releasing factor receptor (CRF-R) encoded by a nucleic acid
CC expression vector, or a cell line containing a nucleic acid vector
CC encoding a recombinant CRF-R. The vector encodes human CRF-R, subtype A,
CC variant 1 (hCRF-RAL). Also included is expressing a recombinant CRF
CC receptor in a suitable host cell, by expressing the vector, where the
CC nucleic acid encodes CRF-R that binds CRF or nucleic acid degenerate to
CC the naturally occurring nucleic acid. The cell line is useful for
CC expressing hCRF-RAL protein by recombinant techniques and in binding
CC assays using CRF-R which are used for rapidly screening large number of
CC compounds to determine which compounds are capable of binding to CRF-R,
CC and for identifying new CRF-like ligands. The polypeptides expressed by
CC the cell line inhibit CRF binding to CRF-R and can inhibit CRF-induced
CC adrenocorticotropin hormone (ACTH) release in vitro by several cells, and
CC so are useful for reducing high ACTH levels caused by excess CRF, and for
CC treating Cushing's disease, pituitary tumours, Alzheimer's disease, and
CC melancholic depression, anorexia nervosa, chronic stress, alcoholism and
CC hypercortisolemia. The proteins are also useful for treating
CC gastrointestinal disorders such as irritable bowel syndrome,
CC abnormalities such as pre-eclampsia, which occur during pregnancy, to
CC reduce pregnancy-induced complications and increased CRF levels which can
CC otherwise result in excessive release of ACTH. The proteins are also
CC useful for locally treating arthritis and other similar ailments,
CC modulating action of CRF in mammals, treating the pregnancy-related
CC pathological disorders in mammals. The CRF-R polypeptides are used in
CC such areas as the diagnosis and/or treatment of CRF-dependent tumours,
CC enhancing the survival of brain neurons, inducing abortion in livestock
CC and other domesticated animals, inducing twinning in livestock and other
CC domesticated animals. The present sequence represents a splice variant of
CC human corticotropin releasing factor receptor, hCRF-RAL
XX
SQ Sequence 444 AA;

Query Match 100.0%; Score 2381; DB 6; Length 444;
Best Local Similarity 100.0%; Pred. No. 8.9e-245;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGHPQLRLVKALLLGLNPVSASLQDQCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
Db 1 MGGHPQLRLVKALLLGLNPVSASLQDQCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GOLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECOEILNEEKSKVHHVAV 120
Db 61 GOLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECOEILNEEKSKVHHVAV 120

Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNSECOEILNEEKSKVHHVAV 120
QY 121 IINYLGHICISLVALLVAFVFLRLRPGCTHWGQADGALVGVGAPWVGAPQVRRSIRCLR 180
Db 121 IINYLGHICISLVALLVAFVFLRLRPGCTHWGQADGALVGVGAPWVGAPQVRRSIRCLR 180
QY 181 NIIHWNLSAFILRNATFVQVLTMSPEVHQSNGVWCRVLTAAAYNFHVTNPFWMFGECC 240
Db 181 NIIHWNLSAFILRNATFVQVLTMSPEVHQSNGVWCRVLTAAAYNFHVTNPFWMFGECC 240
QY 241 YLHTAIVLTYSTDLRKWMPICIGWVPPPIIYVAVAGIKLYDNEKWCWFKRGVGVTDYI 300
Db 241 YLHTAIVLTYSTDLRKWMPICIGWVPPPIIYVAVAGIKLYDNEKWCWFKRGVGVTDYI 300
QY 301 YQGPMLVLLINFILFNIRVILMTKLRASTTSETIQYKAVKATVLLPLLGITVYMLFF 360
Db 301 YQGPMLVLLINFILFNIRVILMTKLRASTTSETIQYKAVKATVLLPLLGITVYMLFF 360
QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVSASIRKRWHRWQDKHSIRARV 420
Db 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVSASIRKRWHRWQDKHSIRARV 420
QY 421 ARAMSIPTSPTRVSHSIRKOSTAV 444
Db 421 ARAMSIPTSPTRVSHSIRKOSTAV 444

RESULT 6
ID ADE62734 standard; protein; 444 AA.
XX
AC ADE62734;
XX
XX 29-JAN-2004 (first entry)
XX
DE Human Protein P34998, SEQ ID NO 8667.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX
XX 01-NOV-2001; 2001US-0346382P.
XX
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GEO) GEN HOSPITAL CORP.
XX
XX (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX
XX GENBANK; P34998.

PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 444 AA;

Query Match 100.0%; Score 2381; DB 7; Length 444;
Best Local Similarity 100.0%; Pred. No. 8.9e-245;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGHPQLRLVKALLLGLNPNVSASLQDHCELSLASNISGLQCNASVDLIGTCWPRSPA 60
Db 1 MGGHPQLRLVKALLLGLNPNVSASLQDHCELSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNSECOEILNEEKSKVHHVAV 120
Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNSECOEILNEEKSKVHHVAV 120
QY 121 IINYLGHICISLVALLVAFVFLRLRPGCTHWGQADGALVGVGAPWVGAPQVRRSIRCLR 180
Db 121 IINYLGHICISLVALLVAFVFLRLRPGCTHWGQADGALVGVGAPWVGAPQVRRSIRCLR 180
QY 181 NIIHWNLSAFILRNATFVQVLTMSPEVHQSNGVWCRVLTAAAYNFHVTNPFWMFGECC 240
Db 181 NIIHWNLSAFILRNATFVQVLTMSPEVHQSNGVWCRVLTAAAYNFHVTNPFWMFGECC 240
QY 241 YLHTAIVLTYSTDLRKWMPICIGWVPPPIIYVAVAGIKLYDNEKWCWFKRGVGVTDYI 300
Db 241 YLHTAIVLTYSTDLRKWMPICIGWVPPPIIYVAVAGIKLYDNEKWCWFKRGVGVTDYI 300
QY 301 YQGPMLVLLINFILFNIRVILMTKLRASTTSETIQYKAVKATVLLPLLGITVYMLFF 360
Db 301 YQGPMLVLLINFILFNIRVILMTKLRASTTSETIQYKAVKATVLLPLLGITVYMLFF 360
QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVSASIRKRWHRWQDKHSIRARV 420
Db 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVSASIRKRWHRWQDKHSIRARV 420
QY 421 ARAMSIPTSPTRVSHSIRKOSTAV 444
Db 421 ARAMSIPTSPTRVSHSIRKOSTAV 444

RESULT 7
ADJ65810
ID ADJ65810 standard; protein; 444 AA.
XX
AC ADJ65810;
XX
XX 20-MAY-2004 (first entry)
XX Human corticotropin-releasing factor receptor CRF-RA2.
XX Human; corticotropin-releasing factor receptor; CRF-RA2; ss; gene;
KW Alzheimer's disease; melancholic depression; anorexia nervosa;
KW Cushing's disease; hypercortisolemia; alcoholism;

KW gastrointestinal disorder; irritable bowel syndrome; inflammation;
 KW Addison's disease; cardiac perfusion; blood pressure; hypotension.
 XX
 OS Homo sapiens.
 XX

FN US2004039173-A1.

XX 26-FEB-2004.

XX 26-AUG-2003; 2003US-00649193.

XX 18-JUN-1993; 93US-00079320.

PR 23-AUG-1993; 93US-00110286.

PR 25-MAY-1994; 94WO-US005908.

PR 09-DEC-1994; 94US-00353537.

PR 07-JUN-1995; 95US-00483139.

PR 12-NOV-1998; 98US-00191724.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

XX Perrin MH, Chen R, Lewis KA, Vale WM, Donaldson CJ, Sawchenko P;

XX WPI; 2004-203293/19.

DR N-PSDB; ADJ65809.

XX New mammalian G protein-coupled corticotropin-releasing factor receptor
 PT protein, useful in diagnosing and treating Alzheimer's disease, anorexia
 PT nervosa, Cushing's disease, alcoholism, irritable bowel syndrome or
 PT hypotension.

XX Claim 7; SEQ ID NO 15; 44pp; English.

XX The invention relates to an isolated mammalian G protein-coupled
 CC corticotropin-releasing factor (CRF) receptor protein or polypeptide from
 CC Rat, Mouse or human appearing as ADJ65801, ADJ65803, ADJ65805, or
 CC ADJ65810, encoded by the nucleic acids appearing as ADJ65800, ADJ65802,
 CC ADJ65804, or ADJ65809. Also included are a composition comprising CRF-R,
 CC an antibody generated against CRF-R and a diagnostic kit, for assaying
 CC for the presence in biological fluids of CRF-R protein, protein analogues
 CC and/or fragments, comprising CRF-R and/or one or more antibodies. The
 CC protein, polynucleotide or composition is useful in diagnosing and
 CC treating Alzheimer's disease, melancholic depression, anorexia nervosa,
 CC Cushing's disease, hypercortisolemia or alcoholism, gastrointestinal
 CC disorders (e.g. irritable bowel syndrome) or physiological conditions
 CC (e.g. inflammation or Addison's disease), in regulating cardiac perfusion
 CC and in modulating blood pressure, thus combat hypotension. The present
 CC sequence represents human splice variant CRF-RA2.

XX Sequence 444 AA;

Query Match 100.0%; Score 2381; DB 8; Length 444;
 Best Local Similarity 100.0%; Pred. No. 8.9e-245;
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGHPQLRLVALLLGLLPVSLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60

DB 1 MGGHPQLRLVALLLGLLPVSLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60

QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHYHVAV 120

DB 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHYHVAV 120

QY 121 IINYLGHCTSLVALLVAFVFLRLPGCTHWGDQADGALEVGAPWPGAPQVRRSRICLR 180

DB 121 IINYLGHCTSLVALLVAFVFLRLPGCTHWGDQADGALEVGAPWPGAPQVRRSRICLR 180

QY 181 NIHNWNLISAFILRNATFVVLQVLTMSPEVHQSNVGCRLVTAAYNYFHTNFFMFEGEC 240

DB 181 NIHNWNLISAFILRNATFVVLQVLTMSPEVHQSNVGCRLVTAAYNYFHTNFFMFEGEC 240

QY 241 YLHTAIVLTYSTDLRKWPFICIGWGPFFIIVAMAIGKYDNEKWCWFKPGVYTDYI 300

DB 241 YLHTAIVLTYSTDLRKWPFICIGWGPFFIIVAMAIGKYDNEKWCWFKPGVYTDYI 300

QY 301 YQGPMLVLLINFIPLFNIVRILMTKLRASSTSETIOYRKAVKATVLLPLIGITYMLFF 360
 DB 301 YQGPMLVLLINFIPLFNIVRILMTKLRASSTSETIOYRKAVKATVLLPLIGITYMLFF 360
 QY 361 VNPGEDEVSRVVIYFNSEFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
 DB 361 VNPGEDEVSRVVIYFNSEFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
 QY 421 ARAMSIPPTSPTRVSVFHSIKQSTAV 444
 DB 421 ARAMSIPPTSPTRVSVFHSIKQSTAV 444

RESULT 8

ADC86255

ID ADC86255 standard; protein; 447 AA.

XX

AC ADC86255;

XX

DT 01-JAN-2004 (first entry)

XX

DE Human GPCR protein SEQ ID NO:708.

XX

KW human; GPCR; guanosine triphosphate-binding protein coupled receptor;

XX gene therapy.

XX

OS Homo sapiens.

XX

PN EP1270724-A2.

XX

XX 02-JAN-2003.

XX

PF 18-JUN-2002; 2002EP-00013517.

XX

PR 18-JUN-2001; 2001JP-00246789.

XX

PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

XX

PI Suwa M, Asai K, Akiyama Y, Aburatani H;

XX WPI; 2003-315783/31.

DR N-PSDB; ADC86254.

XX

PT New polynucleotide, useful for preparing a composition for treating a

PT patient in need of increased or suppressed activity or expression of the

PT guanosine triphosphate-binding protein coupled receptor.

XX

PS Claim 2; SEQ ID NO 708; 28pp; English.

XX

CC The invention relates to a novel polynucleotide encoding a guanosine

CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of

CC the invention may have a use in gene therapy. The polynucleotide and

CC polypeptide are useful for preparing a composition for treating a patient

CC in need of increased or suppressed activity or expression of the

CC guanosine triphosphate-binding protein coupled receptor. The protein

CC sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.

XX

SQ Sequence 447 AA;

Query Match 97.6%; Score 2324; DB 7; Length 447;

Best Local Similarity 99.8%; Pred. No. 1.1e-238;

Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 KALLLGLNPFVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPAGQLVVRPCPA 70

DB 14 RALLLGLNPFVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPAGQLVVRPCPA 73

QY 71 PFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHYHVAVIINYLGHGIS 130

DB 74 PFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHYHVAVIINYLGHGIS 133

[illegible]

RESULT 9
AAR69519
ID AAR69519 standard: protein: 415 AA.

XX	AAR69519;
AC	
XX	
XX	25-MAR-2003 (revised)
DT	21-AUG-1995 (first entry)
XX	
XX	Human pituitary corticotropin releasing factor receptor CRP-RA1.
DE	
XX	Pituitary; hormone; corticotropin releasing factor receptor;
KW	hypothalamus; adrenocorticotrophic hormone; ACTH; Cushing's disease
KW	pituitary tumor; diagnosis.
XX	
OS	Homo sapiens.

Key	Location/Qualifiers
Modified-site	38
Modified-site	/note= "glycosylation site"
Modified-site	45
Modified-site	/note= "glycosylation site"
Modified-site	78
Modified-site	/note= "glycosylation site"
Modified-site	90
Modified-site	/note= "glycosylation site"
Modified-site	98
Modified-site	/note= "glycosylation site"
Modified-site	146
Modified-site	/note= "protein-kinase-C phosphorylation site"
Modified-site	222
Modified-site	/note= "protein-kinase-C phosphorylation site"
Modified-site	301
Modified-site	/note= "casein-kinase-II phosphorylation site"
Modified-site	302
Modified-site	/note= "protein-kinase-A phosphorylation site"
Modified-site	386
Modified-site	/note= "protein-kinase-C phosphorylation site"
Modified-site	408
Modified-site	/note= "protein-kinase-C phosphorylation site"

PN WO9500640-A1.

05-JAN-1995.

AA
PF 25-MAY-1994: 94WO-US005908.

AA 18-JUN-1993; 93US-00079320. PR

PR	23-AUG-1993;	93US-00110286.
XX		
XX	(SALK)	SALK INST BIOLOGICAL STUDIES.
PA		
XX	Perrin MH,	Chen R, Lewis KA, Vale WW, Donaldson CJ;
PI		
XX	WPI;	1995-052077/07.
DR	N-PSDB;	AAQ81952.
DR		
XX	Isolated	corticotropin releasing factor receptor and nucleic acid - also
PT	antibodies,	useful for diagnosis and treatment of Cushing's disease,
PT	pituitary	tumours etc., also to identify specific agonists and
PT	antagonists.	
XX		
XX	Claim 3;	Page 65; 84pp; English.
PS		
XX		
CC	This	protein can be used to determine CRF (e.g. over- or under-
CC	production,	high levels of CRF late in pregnancy may indicate risk of
CC	premature	labor). Cells expressing the protein are used to identify e.g.
CC	antibodies,	which can be used to modulate signal transduction activity
CC	mediated	by CRF receptors. Typical applications are in the treatment of
CC	Cushing's	disease, pituitary tumors, etc. (Updated on 25-MAR-2003 to
CC	correct	PN field.)
XX		
XX	Sequence	415 AA;
SO		

Query Match		91.8%; Score 2186.5; DB 2; Length 415;
Best local similarity		93.5%; Pred. No. 4.8e-224;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;		
Qy	1	MGGHPQLRLVKALLLGLNPVSASLOQHCHESLSLASNIGLCQNASVDLIGTCWPRSPA 60
Dd	1	MGGHPQLRLVKALLLGLNPVSASLOQHCHESLSLASNIGLCQNASVDLIGTCWPRSPA 60
Qy	61	GQLVVRPCPAFFYGVGYRNTTNNGRYRECLANGSWAARVNTSECOILNEEKSKXVHHVV 120
Dd	61	GQLVVRPCPAFFYGVGYRNTTNNGRYRECLANGSWAARVNTSECOILNEEKSKXVHHVV 120
Qy	121	IINYLGHICISLVALLVAFLFLRLRPCTHGWGDQALEVGAPWGAPPQVRRSRIRCLR 180 -----RSIRCLR 151
Dd	121	IINYLGHICISLVALLVAFLFLRL-----RSIRCLR 151 -----RSIRCLR 151
Qy	181	NIIHWNLISAPIURNATWFVVQLTMSPEVHQSNVGCRLVTAAINYTFHVNTPFWMFGECC 240
Dd	152	NIIHWNLISAFILRNATWFVVQLTMSPEVHQSNVGCRLVTAAINYTFHVNTPFWMFGECC 211
Qy	241	YLHTAVLTYSTDLRAKRWEIFCI GWGVPPPIIVAWAIGKLYDNEKCWCGRPGCVYTDIYI 300
Dd	212	YLHTAVLTYSTDLRAKRWEIFCI GWGVPPPFIIVAWAIGKLYDNEKCWCGRPGCVYTDIYI 271
Qy	301	YQGPMILLVLLINEIFLFNI VRIIMTKLRASTSETTIQYRKAVKATLVLLPLLGITYMLFF 360
Dd	272	YQGPMILLVLLINEIFLFNI VRIIMTKLRASTSETTIQYRKAVKATLVLLPLLGITYMLFF 331
Qy	361	VNPGEDEVSRVPFIYNFSFLESFGGFVSVFYCFLNSEVESAIKRKHWRHWDKHSIRARV 420
Dd	332	VNPGEDEVSRVPFIYNFSFLESFGGFVSVFYCFLNSEVESAIKRKHWRHWDKHSIRARV 391
Qy	421	ARAMSPTSPTRVSFHSIKOSTAV 444
Dd	392	ARAMSPTSPTRVSFHSIKOSTAV 415

RESULT 10
AAR97290
ID AAR97290 standard; protein; 415 AA.
XX
XX
AC AAR97290;
XX
XX 21-AUG-1996 (first entry)
DT XX
XX
DE Human CRF receptor CRF-R1.
XX
XX

KW Corticotropin releasing factor receptor; CRF-R; corticoliberin;
 XX signal transduction.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 38 /label= N-glycosylation_site

FT Modified-site 45 /label= N-glycosylation_site

FT Modified-site 78 /label= N-glycosylation_site

FT Modified-site 90 /label= N-glycosylation_site

FT Modified-site 98 /label= N-glycosylation_site

FT Modified-site 146 /label= N-glycosylation_site

FT Modified-site 222 /label= Phosphorylation site

FT Modified-site 301 /label= "protein kinase C phosphorylation site"

FT Modified-site 302 /label= "casein kinase II phosphorylation site"

FT Modified-site 386 /label= "protein kinase A phosphorylation site"

FT Modified-site 408 /label= "protein kinase C phosphorylation site"

FT Modified-site 408 /label= "protein kinase C phosphorylation site"

FT Modified-site 408 /label= "protein kinase C phosphorylation site"

FT Modified-site 408 /label= "protein kinase C phosphorylation site"

FT Modified-site 408 /label= "protein kinase C phosphorylation site"

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FT Modified-site 408 /label= "protein kinase C phosphorylation site"

FT Modified-site 408 /label= "protein kinase C phosphorylation site"

FT Modified-site 408 /label= "protein kinase C phosphorylation site"

XX Sequence 415 AA;

Query Match

Best Local Similarity 91.8%; Score 2186.5; DB 2; Length 415;

Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY 1 MGHPQLRLVKALLLGLNPNVSLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
 DB 1 MGHPQLRLVKALLLGLNPNVSLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
 QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHYHVA 120
 DB 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHYHVA 120
 QY 121 IINYLGHCSISVALLVAVFLRLRPGCTHWGDQDGALEVPWGSAPFQVRRSTRCLR 180
 DB 121 IINYLGHCSISVALLVAVFLRLRPGCTHWGDQDGALEVPWGSAPFQVRRSTRCLR 180
 QY 181 NIIHWNLISAFILRNATFWVOLTMSPEVHQSNVGMCRVLTAAVNYFHVTFNFMFGECC 240
 DB 181 NIIHWNLISAFILRNATFWVOLTMSPEVHQSNVGMCRVLTAAVNYFHVTFNFMFGECC 240
 QY 241 YLHTAIVLTYSTDLRLKWMFICIGWGPPIIIVAMAIGKLYYDNEKWFGRPGVYTDYI 300
 DB 241 YLHTAIVLTYSTDLRLKWMFICIGWGPPIIIVAMAIGKLYYDNEKWFGRPGVYTDYI 300
 QY 301 YQGPMLILVLLINFIENIVIRILMTKLRASITSETIQYRKAVKATLVLLPLIGITVMLFP 360
 DB 301 YQGPMLILVLLINFIENIVIRILMTKLRASITSETIQYRKAVKATLVLLPLIGITVMLFP 360
 QY 361 VNPGEDEVSRVVFYFNSFLESFQGFVSVFVCFNLSVRSVSAIRKRWQDKHSIRARV 420
 DB 361 VNPGEDEVSRVVFYFNSFLESFQGFVSVFVCFNLSVRSVSAIRKRWQDKHSIRARV 420
 QY 421 ARAMSIPTSPTRVSPHSIKQSTAV 444
 DB 421 ARAMSIPTSPTRVSPHSIKQSTAV 444
 RESULT 11
 AAW00159
 ID AAW00159 standard; protein; 415 AA.
 AC AAW00159;
 XX 16-OCT-1996 (first entry)
 DT Human corticotropin releasing factor receptor protein.
 DE Human; corticotropin releasing factor; CRF; receptor; expression vector;
 KW PACO2; agonist; antagonist; blood pressure; immunosuppression.
 OS Homo sapiens.
 XX JP08140680-A.
 PN 04-JUN-1996.
 PD 22-NOV-1994; 94JP-00287638.
 PF 22-NOV-1994; 94JP-00287638.
 PR (TAKE) TAKEDA CHEM IND LTD.
 PA WPI; 1996-316316/32.
 DR N-PSDB; AAT37068.
 XX Recombinant human corticotropin releasing factor receptor protein -
 PT useful to screen for (ant)agonist for lowering blood pressure, as a
 PT gastrointestinal regulator and for treatment of immunosuppression.
 XX Claim 1; Fig 1; 2ipp; Japanese.
 CC This sequence represents human corticotropin releasing factor (CRF)
 CC receptor protein. The cDNA fragment is derived from the expression vector
 CC designated PACO2. PACO2 is an expression vector constructed for elevated
 CC expression of the human CRF receptor protein. The recombinantly produced
 CC CRF receptor protein or a peptide fragment, may be used for efficient and
 CC rapid screening of an agonist or antagonist of human CRF receptor.

CC Agonists may be used for lowering blood pressure, and antagonists may be
CC used for the treatment of immunosuppression
XX
SQ Sequence 415 AA;

Query Match 91.8%; Score 2186.5; DB 2; Length 415;
Best Local Similarity 93.5%; Pred. No. 4.8e-224;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY 1 MGGHPQLRLVKALLLGLNLPVSASLQDQHCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGGHPQLRLVKALLLGLNLPVSASLQDQHCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHYHVAV 120
DB 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHYHVAV 120
QY 121 IINYLGHCSLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWSPAPQVRRSIRCLR 180
DB 121 IINYLGHCSLVALLVAFVFLRLR-----RSIRCLR 151
QY 181 NIIHWNLSAFILRNATFWVQLTMSPEVHQSNVGMCRLVTAAYNYFHVTFNFFMFGEGC 240
DB 152 NIIHWNLSAFILRNATFWVQLTMSPEVHQSNVGMCRLVTAAYNYFHVTFNFFMFGEGC 211
QY 241 YLHTAIVLTSTDRLRKWMFCIGWGVPPIIIVAWAIGKLYYDNEKCFQKRGVYTDYI 300
DB 212 YLHTAIVLTSTDRLRKWMFCIGWGVPPIIIVAWAIGKLYYDNEKCFQKRGVYTDYI 271
QY 301 YQGPMLVLLINFIPLNVIIRILMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF 360
DB 272 YQGPMLVLLINFIPLNVIIRILMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF 331
QY 361 VNPGEDEVSRVFIYFNSFLESFGFVSVFYCFNLSEVSARVKRHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVFIYFNSFLESFGFVSVFYCFNLSEVSARVKRHRWQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSHSIKOSTAV 444
DB 392 ARAMSIPTSPTRVSHSIKOSTAV 415

RESULT 12
AAE26679
ID AAE26679 standard; protein; 415 AA.
AC AAE26679;
XX
DT 13-DEC-2002 (first entry)
DE Human CRF-RA1 protein.
XX
KW Human; G protein-coupled corticotropin-releasing factor receptor; CRF;
KW CRF-R; adrenocorticotrophic hormone; irritable bowel syndrome; therapy;
KW Cushing's syndrome; pituitary tumour; chronic stress; anorexia nervosa;
KW receptor; alcoholism; CRF-RA1.
XX
OS Homo sapiens.
XX
PN US2002055617-A1.
PD 09-MAY-2002.
XX
PF 12-NOV-1998; 98US-00191724.
XX
PR 18-JUN-1993; 93US-00079320.
PR 23-AUG-1993; 93US-00110286.
PR 25-MAY-1994; 94WO-US005908.
PR 09-DEC-1994; 94US-00353537.
PR 07-JUN-1995; 95US-00483139.
XX
PA (PERR/) PERRIN M H.
PA (CHEN/) CHEN R.

PA (LEW/) LEWIS X A.
PA (VALE/) VALE W W.
PA (DONA/) DONALDSON C J.
PA (SAWC/) SAWCHENKO P.
XX
PI Perrin MH, Chen R, Lewis KA, Vale WW, Donaldson CJ, Sawchenko P;
XX WPI; 2002-462916/49.
DR N-PSDB; AAD44482.
XX
XX New isolated recombinant mammalian G protein-coupled corticotropin-
PT releasing factor receptor protein for treating e.g. Cushing's syndrome,
PT pituitary tumors, stress, anorexia, alcoholism or irritable bowel
PT syndrome.
XX
PS Claim 4; Page 22-23; 44pp; English.
XX
XX The invention relates to recombinant mammalian G protein-coupled
CC corticotropin-releasing factor (CRF) receptor (CRF-R) proteins having
CC high affinity for CRF and nucleic acid molecules encoding such receptor
CC proteins. Polypeptides of the invention can be used to reduce high levels
CC of adrenocorticotrophic hormone caused by excess CRF and so can be used
CC to treat diseases such as Cushing's syndrome, pituitary tumours, chronic
CC stress, anorexia nervosa, alcoholism and irritable bowel syndrome. They
CC are used in pharmaceuticals and in the production of antibodies. The
CC present sequence is human CRF-RA1 protein
XX
SQ Sequence 415 AA;

Query Match 91.8%; Score 2186.5; DB 5; Length 415;
Best Local Similarity 93.5%; Pred. No. 4.8e-224;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY 1 MGGHPQLRLVKALLLGLNLPVSASLQDQHCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGGHPQLRLVKALLLGLNLPVSASLQDQHCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHYHVAV 120
DB 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHYHVAV 120
QY 121 IINYLGHCSLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWSPAPQVRRSIRCLR 180
DB 121 IINYLGHCSLVALLVAFVFLRLR-----RSIRCLR 151
QY 181 NIIHWNLSAFILRNATFWVQLTMSPEVHQSNVGMCRLVTAAYNYFHVTFNFFMFGEGC 240
DB 152 NIIHWNLSAFILRNATFWVQLTMSPEVHQSNVGMCRLVTAAYNYFHVTFNFFMFGEGC 211
QY 241 YLHTAIVLTSTDRLRKWMFCIGWGVPPIIIVAWAIGKLYYDNEKCFQKRGVYTDYI 300
DB 212 YLHTAIVLTSTDRLRKWMFCIGWGVPPIIIVAWAIGKLYYDNEKCFQKRGVYTDYI 271
QY 301 YQGPMLVLLINFIPLNVIIRILMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF 360
DB 272 YQGPMLVLLINFIPLNVIIRILMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF 331
QY 361 VNPGEDEVSRVFIYFNSFLESFGFVSVFYCFNLSEVSARVKRHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVFIYFNSFLESFGFVSVFYCFNLSEVSARVKRHRWQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSHSIKOSTAV 444
DB 392 ARAMSIPTSPTRVSHSIKOSTAV 415

RESULT 13
AAO19420
ID AAO19420 standard; protein; 415 AA.
XX
AC AAO19420;
XX
DT 10-DEC-2002 (first entry)

XX DE Human corticotrophin releasing factor receptor CRF1R.
XX KW Human; rat; mouse; sheep; cow; chicken; CRF1R; CRF2R;
KW skeletal muscle atrophy; corticotrophin releasing factor-2 receptor;
KW muscular dystrophy; corticotrophin releasing factor-1 receptor;
XX KW gene therapy.
XX OS Homo sapiens.
XX PN WO200269908-A2.
XX PD 12-SEP-2002.
XX PF 06-MAR-2002; 2002WO-US007476.
XX PR 06-MAR-2001; 2001US-00799978.
XX PA (PROC) PROCTER & GAMBLE CO.
XX PI Isfort RJ, Sheldon RJ;
XX DR WPI; 2002-713413/77.
XX DR N-PSDB; AAL49971.
XX PT Identifying candidate compounds for regulating skeletal muscle mass or
PT treating skeletal muscle atrophy by identifying test compounds that bind
PT to, or activate, the corticotrophin releasing factor-2 receptor.
XX PS Disclosure; Page 79-80; 167pp; English.
XX CC The present invention relates to a method of identifying candidate
CC compounds for regulating skeletal muscle mass or function, and comprises
CC contacting a test compound with a corticotropin releasing factor-2
CC receptor (CRF2R) or with a cell expressing a functional CRF2R,
CC determining whether the test compound binds to, or activates, the CRF2R
CC and identifying the test compounds that bind to, or activates, the CRF2R
CC as candidate compounds for regulating skeletal muscle mass or function.
CC The method is useful for preparing a medicament for treating skeletal
CC muscle atrophy or for prophylactic treatment of muscular dystrophies. The
CC present sequence is a corticotrophin releasing factor receptor
XX SQ Sequence 415 AA;
Query Match 91.8%; Score 2186.5; DB 5; Length 415;
Best Local Similarity 93.5%; Pred. No. 4.8e-224;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;
QY 1 MGGHPQLRLVKALLLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGGHPQLRLVKALLLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCPAFFGVRVNTTNGVRECLANGSWAARVNYSECQEIILNEEKSKVHYHVAV 120
DB 61 GQLVVRPCPAFFGVRVNTTNGVRECLANGSWAARVNYSECQEIILNEEKSKVHYHVAV 120
QY 121 IINYLGHICISLVALLVAFVLFLRLPCTGWDQADGALEVPWPGAPQVRRSIRCLR 180
DB 121 IINYLGHICISLVALLVAFVLFLRLPCTGWDQADGALEVPWPGAPQVRRSIRCLR 151
QY 181 NIHWNLISAFILRNATWVFVQLTMSPEVHQSNGWCRVLTAAVNYFHVNTFFWMEGEC 240
DB 152 NIHWNLISAFILRNATWVFVQLTMSPEVHQSNGWCRVLTAAVNYFHVNTFFWMEGEC 211
QY 241 YLHTAIVLTSTDRLRKWMFCIGWGVPFPIIVAWAIGKLYDNEKCMFKRGVYTDYI 300
DB 212 YLHTAIVLTSTDRLRKWMFCIGWGVPFPIIVAWAIGKLYDNEKCMFKRGVYTDYI 271
QY 301 YQSPMLVLLINIFLNIYRIILMTKLRASTSTETQYRKAVKATVLLPLLGITVMLFF 360
DB 272 YQSPMLVLLINIFLNIYRIILMTKLRASTSTETQYRKAVKATVLLPLLGITVMLFF 331
QY 361 VNPGEDEVSRVVFYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420

DB 332 VNPGEDEVSRVVFYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSPHSIKQSTAV 444
DB 392 ARAMSIPTSPTRVSPHSIKQSTAV 415
RESULT 14
AAO19421
ID AAO19421 standard; protein; 415 AA.
XX AC AAO19421;
XX DT 10-DEC-2002 (first entry)
XX DE Human corticotrophin releasing factor receptor CRF1R variant.
XX KW Human; rat; mouse; sheep; cow; chicken; CRF1R; CRF2R;
KW skeletal muscle atrophy; corticotrophin releasing factor-2 receptor;
KW muscular dystrophy; corticotrophin releasing factor-1 receptor;
XX KW gene therapy.
XX OS Homo sapiens.
XX PN WO200269908-A2.
XX PD 12-SEP-2002.
XX PF 06-MAR-2002; 2002WO-US007476.
XX PR 06-MAR-2001; 2001US-00799978.
XX PA (PROC) PROCTER & GAMBLE CO.
XX PI Isfort RJ, Sheldon RJ;
XX DR WPI; 2002-713413/77.
XX DR N-PSDB; AAL49972.
XX PT Identifying candidate compounds for regulating skeletal muscle mass or
PT treating skeletal muscle atrophy by identifying test compounds that bind
PT to, or activate, the corticotrophin releasing factor-2 receptor.
XX PS Disclosure; Page 83-84; 167pp; English.
XX CC The present invention relates to a method of identifying candidate
CC compounds for regulating skeletal muscle mass or function, and comprises
CC contacting a test compound with a corticotropin releasing factor-2
CC receptor (CRF2R) or with a cell expressing a functional CRF2R,
CC determining whether the test compound binds to, or activates, the CRF2R
CC and identifying the test compounds that bind to, or activates, the CRF2R
CC as candidate compounds for regulating skeletal muscle mass or function.
CC The method is useful for preparing a medicament for treating skeletal
CC muscle atrophy or for prophylactic treatment of muscular dystrophies. The
CC present sequence is a corticotrophin releasing factor receptor
XX SQ Sequence 415 AA;
Query Match 91.8%; Score 2186.5; DB 5; Length 415;
Best Local Similarity 93.5%; Pred. No. 4.8e-224;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;
QY 1 MGGHPQLRLVKALLLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGGHPQLRLVKALLLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCPAFFGVRVNTTNGVRECLANGSWAARVNYSECQEIILNEEKSKVHYHVAV 120
DB 61 GQLVVRPCPAFFGVRVNTTNGVRECLANGSWAARVNYSECQEIILNEEKSKVHYHVAV 120
QY 121 IINYLGHICISLVALLVAFVLFLRLPCTGWDQADGALEVPWPGAPQVRRSIRCLR 180
DB 121 IINYLGHICISLVALLVAFVLFLRLPCTGWDQADGALEVPWPGAPQVRRSIRCLR 151

Db 121 IINVLGHICISLVALLVAFVLFRL-----RSIRCLR 151
Qy 181 NIIHWNLSAFILRNATWVQVLTMSPEVHQSNGVCLVTAAYNYFHVTFNPFMFGECC 240
Db 152 NIIHWNLSAFILRNATWVQVLTMSPEVHQSNGVCLVTAAYNYFHVTFNPFMFGECC 211
Qy 241 YLHTAIVLTYSTDLRKKWFCIGWGVPPFIIVAWAIGKLYYDNEKCFWGRPGVYTDYI 300
Db 212 YLHTAIVLTYSTDLRKKWFCIGWGVPPFIIVAWAIGKLYYDNEKCFWGRPGVYTDYI 271
Qy 301 YQGPMLVLLINFIPLFNIVRLMTKLRASTTSETIOYRKAVKATLVLLPLLGITYMLFF 360
Db 272 YQGPMLVLLINFIPLFNIVRLMTKLRASTTSETIOYRKAVKATLVLLPLLGITYMLFF 331
Qy 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFLNSEVRSIAIKRWHRWQDHSIRARV 420
Db 332 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFLNSEVRSIAIKRWHRWQDHSIRARV 391
Qy 421 ARAMSIPTSPTRVSEHSIKOSTAV 444
Db 392 ARAMSIPTSPTRVSEHSIKOSTAV 415

RESULT 15

ABG66957
ID ABG66957 standard; protein; 415 AA.

XX AC ABG66957;
XX

DT 24-SEP-2002 (first entry)
XX

DE Human corticotrophin releasing hormone.
XX

KW Yeast; G-Protein Coupled Receptor; GPCR-regulated signaling pathway;
KW GPCR; sxa2 promoter; Galpha-transplant; Galphaq; Galphas; Galphaz;
KW Galphai2; Galphai3; Galphaz; Galphai2; Galphai3; Galphai4; Galphai6;
KW receptor.
XX

OS Homo sapiens.
XX

XX W0200246369-A2.
XX

XX 13-JUN-2002.
XX

XX 10-DEC-2001; 2001WO-GB005460.
XX

XX 08-DEC-2000; 2000GB-00030038.
XX

XX (SEPT-) SEPTGEN LTD.
XX

XX Davey J;
XX

XX WPI; 2002-508557/54.
XX

XX N-PSDB; ABK95583.
XX

PT New Schizosaccharomyces pombe cell, useful for studying G-protein coupled
PT receptor-regulated activity, comprises receptor-regulated signaling
PT pathway that is derepressed during cell growth mitotic phase and
PT reporter.
XX

XX Disclosure; Page 85-87; 117pp; English.
XX

XX The invention relates to a Schizosaccharomyces pombe yeast cell (1)
XX comprising: (a) a heterologous G-Protein Coupled Receptor (GPCR)-
XX regulated signaling pathway (P1) which is derepressed during mitotic
XX phase of cell growth; and (b) a reporter system (RS) for reporting signal
XX mediated by P1, where RS has reporter gene (G1) operatively linked to
XX promoter (PR), which is regulatable by GPCR, and G1 and PR is
XX heterologous. Also described is (1) an isolated polynucleotide (Iia)
XX comprising an sxa2 promoter, or its homologue or analogue, operatively
XX linked to an exogenous reporter gene; (2) an isolated polynucleotide
XX (Iib) encoding a Galpha-transplant having a nucleotide sequence from
XX Galphaq, Galphas, Galphaz, Galphai2, Galphai3, Galphas, Galphai2,

CC Galphai3, Galphai4 and Galphai6. (1), (Iia) or (Iib) is useful for
CC studying GPCR-regulated activity, for determining the effect of a
CC compound on GPCR-regulated activity by introducing the compound, to (1)
CC and noting the output of RS, where the compound affects the ability of
CC orphan GPCR to regulate RS. Furthermore (1) is useful for identifying a
CC regulator or a mutant of a component of GPCR-regulated pathway and for
CC identifying a reagent that modulates GPCR-regulated signaling pathways,
CC by producing a random peptide within (1) and measuring an amount of
CC reporter activity produced. ABK95570-ABK95608 represent Galpha-
CC transplant amino acid sequences and related amino acid sequences of the
CC invention
XX
SQ Sequence 415 AA;

Query Match 91.8%; Score 2186.5; DB 5; Length 415;
Best Local Similarity 93.5%; Pred. No. 4.8e-224;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

Qy 1 MGGHPQLRLVKALLLGLNPNVSASLODHCELSLASNISGLQCNASVDLIGTCWPRSPA 60
Db 1 MGGHPQLRLVKALLLGLNPNVSASLODHCELSLASNISGLQCNASVDLIGTCWPRSPA 60
Qy 61 GOLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQILNEEKSKVHYHVAV 120
Db 61 GOLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQILNEEKSKVHYHVAV 120
Qy 121 IINVLGHICISLVALLVAFVLFRL-----RSIRCLR 180
Db 121 IINVLGHICISLVALLVAFVLFRL-----RSIRCLR 151
Qy 181 NIIHWNLSAFILRNATWVQVLTMSPEVHQSNGVCLVTAAYNYFHVTFNPFMFGECC 240
Db 152 NIIHWNLSAFILRNATWVQVLTMSPEVHQSNGVCLVTAAYNYFHVTFNPFMFGECC 211
Qy 241 YLHTAIVLTYSTDLRKKWFCIGWGVPPFIIVAWAIGKLYYDNEKCFWGRPGVYTDYI 300
Db 212 YLHTAIVLTYSTDLRKKWFCIGWGVPPFIIVAWAIGKLYYDNEKCFWGRPGVYTDYI 271
Qy 301 YQGPMLVLLINFIPLFNIVRLMTKLRASTTSETIOYRKAVKATLVLLPLLGITYMLFF 360
Db 272 YQGPMLVLLINFIPLFNIVRLMTKLRASTTSETIOYRKAVKATLVLLPLLGITYMLFF 331
Qy 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFLNSEVRSIAIKRWHRWQDHSIRARV 420
Db 332 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFLNSEVRSIAIKRWHRWQDHSIRARV 391
Qy 421 ARAMSIPTSPTRVSEHSIKOSTAV 444
Db 392 ARAMSIPTSPTRVSEHSIKOSTAV 415

Search completed: March 16, 2006, 17:16:18
Job time : 195 secs

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OM protein - protein search, using sw model

Run on: March 16, 2006, 17:16:39 ; Search time 41 Seconds
(without alignments)
1041.957 Million cell updates/sec

Title: US-10-649-193-15
Perfect score: 2381
Sequence: 1 MGGHPQLRLVKALLLLGLNP.....SIPTSPTRVSPHSIKQSTAV 444

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2381	100.0	444	2 A48260	corticoliberin rec
2	2137.5	89.8	415	2 S39535	corticotropin-rele
3	2126.5	89.3	415	2 I58144	corticotropin-rele
4	1925.5	80.9	375	2 I38879	corticotropin-rele
5	1550.5	65.1	411	2 A56810	corticotropin-rele
6	1543	64.8	431	2 I49149	CRF receptor - mou
7	1540.5	64.7	430	2 A56726	corticoliberin rec
8	1518.5	63.8	431	2 I49279	sauvagine/corticot
9	565	23.7	585	2 A39286	parathyroid hormon
10	554.5	23.3	593	2 A49191	parathyroid hormon
11	543.5	22.8	591	2 S44203	parathyroid hormon
12	543.5	22.8	591	2 I54195	parathyroid hormon
13	535	22.5	459	2 JH0594	vasoactive intesti
14	533	22.4	498	2 I47130	calcitonin recepto
15	531.5	22.3	449	2 I16319	secretin receptor
16	530	22.3	515	2 I49154	calcitonin recepto
17	527.5	22.2	589	2 I59297	parathyroid hormon
18	524	22.0	482	2 A39285	calcitonin recepto
19	518	21.8	440	2 JC2532	secretin receptor
20	518	21.8	495	2 JC2195	vasoactive intesti
21	513	21.5	490	2 S34486	calcitonin recepto
22	512.5	21.5	515	2 I60800	calcitonin recepto
23	511.5	21.5	479	2 S33746	calcitonin recepto
24	511	21.5	460	2 JC2194	vasoactive intesti
25	510.5	21.4	477	2 JC2041	glucagon recepto
26	510	21.4	474	2 I37217	calcitonin recepto
27	507	21.3	478	2 A37430	calcitonin recepto
28	504.5	21.2	550	2 A57519	parathyroid hormon
29	485.5	20.4	463	2 A46172	glucagon-like pept

30	485.5	20.4	485	2 JQ1957	glucagon receptor
31	483.5	20.3	485	2 JC4363	glucagon receptor
32	478	20.1	463	2 S71624	glucagon-like pept
33	477.5	20.1	464	2 I60194	calcitonin-like re
34	473.5	19.9	461	2 JC2477	calcitonin recepto
35	471.5	19.8	525	2 JN0902	pituitary adenylat
36	468.5	19.7	467	2 JN0616	pituitary adenylat
37	464	19.5	463	2 I84494	glucagon-like pept
38	459.5	19.3	438	2 G02822	vasoactive intesti
39	458.5	19.3	513	2 S47631	pituitary adenylat
40	455	19.1	451	2 I46586	growth hormone-rel
41	451.5	19.0	466	2 S66676	glucose-dependent
42	450.5	18.9	423	2 A45363	somatoliberin rece
43	450.5	18.9	495	2 S36114	pituitary adenylat
44	448.5	18.8	495	2 S39061	pituitary adenylat
45	448	18.8	466	2 G02234	gastric inhibitory

ALIGNMENTS

RESULT 1

A48260
corticoliberin receptor, long splice form - human
N;Alternate names: corticoliberin binding protein; corticotropin releasing factor recepto
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence revision 11-Apr-1997 #text_change 09-Jul-2004
C;Accession: I60975; A48260; S39534
R;Chen, R.; Lewis, K.A.; Perrin, M.H.; Vale, W.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 8967-8971, 1993
A;Title: Expression Cloning of a human corticotropin-releasing factor (CRF) receptor.
A;Reference number: A48260; MUID:94022296; PMID:7692441
A;Accession: I60975
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-444 <RES>
A;Cross-references: UNIPROT:P34998; UNIPARC:UPI0000128429; GB:L23333; NID:9408691; PIDN:?
A;Experimental source: Cushing corticotropic cell tumor
A;Accession: A48260
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-145,175-444 <RE2>
A;Cross-references: UNIPARC:UPI000002A71D; GB:L23332; NID:9408689; PIDN:AAA35718.1; PID:?
R;Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Lelias, J.M.; Kaghad, M.; le Fur, G.; C
FEBS Lett. 335, 1-5, 1993
A;Title: Primary structure and functional expression of mouse pituitary and human brain
A;Reference number: S39534; MUID:94063063; PMID:8243652
A;Accession: S39534
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-145,175-444 <VIT>
A;Cross-references: UNIPARC:UPI000002A71D; EMBL:X72304; NID:9436118; PIDN:CAA51052.1; PFI
A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 3 in having an addit
C;Genetics:
A;Gene: GDB:CHRI; CHR: CRP-R; CRP1
A;Cross-references: GDB:235922; OMIM:122561
A;Map position: 17q12-17q22
C;Superfamily: glucagon receptor
C;Keywords: alternative splicing; transmembrane protein

Query Match	100.0%;	Score 2381;	DB 2;	Length 444;
Best Local Similarity	100.0%;	Pred. No. 4.6e-199;		
Matches 444;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	1	MGGHPQLRLVKALLLLGLNPVSASLODQHCEISLASNISGLQCNASVDLIGTCWPRSPA	60	
Db	1	MGGHPQLRLVKALLLLGLNPVSASLODQHCEISLASNISGLQCNASVDLIGTCWPRSPA	60	
Qy	61	GQLVVRPCPAFFYGVRYNTTNNNGRECLANGSWAARVNYSECQIILNEEKSKVHYHAV	120	
Db	61	GQLVVRPCPAFFYGVRYNTTNNNGRECLANGSWAARVNYSECQIILNEEKSKVHYHAV	120	
Qy	121	IINYLGHCSISVALLVAVFLRLRPGCTHWGDAQDALEVGAPFWGAPQVRRSIRCLR	180	

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Db 121 IINVLGHICISLVALLVAFVFLRLRPGCTHWGQADGALVGPWVGAPQVRSIRCLR 180
QY 181 NIIHWNLISAFILRNATFVQVLTMSPEVHQSNGVWCRLVTAAYNFHVTNPFPMFGEBC 240
Db 181 NIIHWNLISAFILRNATFVQVLTMSPEVHQSNGVWCRLVTAAYNFHVTNPFPMFGEBC 240
QY 241 YLHTAIVLTYSTDRLRKMFVICIGWGPVPIIIVAMAIGKLYYDNEKWCWKGKPGVYTDYI 300
Db 241 YLHTAIVLTYSTDRLRKMFVICIGWGPVPIIIVAMAIGKLYYDNEKWCWKGKPGVYTDYI 300
QY 301 YQGPMILVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITTYMLFF 360
Db 301 YQGPMILVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITTYMLFF 360
QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
Db 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
QY 421 ARAWSIPTSPTRVSPHSIKOSTAV 444
Db 421 ARAWSIPTSPTRVSPHSIKOSTAV 444

RESULT 2
S39535
Corticotropin-releasing hormone receptor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S39535
R/Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Lelias, J.M.; Kaghad, M.; le Fur, G.; C
PBBS Lett. 335, 1-5, 1993
A/Title: Primary structure and functional expression of mouse pituitary and human brain
A/Reference number: S39534; MUID:94063063; PMID:8243652
A/Accession: S39535
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-415 <VT>
A/Cross-references: UNIPROT:P35347; UNIPARC:UPI0000027DE5; EMBL:X72305; NID:g436120; PID
A/Note: the sequence from Fig. 1 is inconsistent with that from Fig. 3 in having an addi
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 89.8%; Score 2137.5; DB 2; Length 415;
Best Local Similarity 91.2%; Pred. No. 6.2e-178; Indels 29; Gaps 1;
Matches 405; Conservative 4; Mismatches 6;

QY 1 MGGHPQLRLVKALLLGLNPNVSASLQDQCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
Db 1 MGQRPQLRLVKALLLGLNPNVSTSLQDQCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECEILNEEKSKKVHYHVAV 120
Db 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECEILNEEKSKKVHYHVAV 120
QY 121 IINVLGHICISLVALLVAFVFLRLRPGCTHWGQADGALVGPWVGAPQVRSIRCLR 180
Db 121 IINVLGHICISLVALLVAFVFLRLRPGCTHWGQADGALVGPWVGAPQVRSIRCLR 180
QY 181 NIIHWNLISAFILRNATFVQVLTMSPEVHQSNGVWCRLVTAAYNFHVTNPFPMFGEBC 240
Db 181 NIIHWNLISAFILRNATFVQVLTMSPEVHQSNGVWCRLVTAAYNFHVTNPFPMFGEBC 240
QY 241 YLHTAIVLTYSTDRLRKMFVICIGWGPVPIIIVAMAIGKLYYDNEKWCWKGKPGVYTDYI 300
Db 241 YLHTAIVLTYSTDRLRKMFVICIGWGPVPIIIVAMAIGKLYYDNEKWCWKGKPGVYTDYI 300
QY 301 YQGPMILVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITTYMLFF 360
Db 301 YQGPMILVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITTYMLFF 360
QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
Db 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420

RESULT 3
I58144
corticotropin-releasing factor receptor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: I58144
R/Chang, C.P.; Pearce, R.V.; O'Connell, S.; Rosenfeld, M.G.
Neuron 11, 1187-1195, 1993
A/Title: Identification of a seven transmembrane helix receptor for corticotropin-releas
A/Reference number: I58144; MUID:94099969; PMID:8274282
A/Accession: I58144
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-415 <RES>
A/Cross-references: UNIPROT:P35353; UNIPARC:UPI000002EF2A; GB:L25438; NID:g450298; PIDN:
C/Superfamily: glucagon receptor

Query Match 89.3%; Score 2126.5; DB 2; Length 415;
Best Local Similarity 90.8%; Pred. No. 5.6e-177; Indels 29; Gaps 1;
Matches 403; Conservative 5; Mismatches 7;

QY 1 MGGHPQLRLVKALLLGLNPNVSASLQDQCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
Db 1 MGRRPQLRLVKALLLGLNPNVSTSLQDQCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECEILNEEKSKKVHYHVAV 120
Db 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECEILNEEKSKKVHYHVAV 120
QY 121 IINVLGHICISLVALLVAFVFLRLRPGCTHWGQADGALVGPWVGAPQVRSIRCLR 180
Db 121 IINVLGHICISLVALLVAFVFLRLRPGCTHWGQADGALVGPWVGAPQVRSIRCLR 180
QY 181 NIIHWNLISAFILRNATFVQVLTMSPEVHQSNGVWCRLVTAAYNFHVTNPFPMFGEBC 240
Db 181 NIIHWNLISAFILRNATFVQVLTMSPEVHQSNGVWCRLVTAAYNFHVTNPFPMFGEBC 240
QY 241 YLHTAIVLTYSTDRLRKMFVICIGWGPVPIIIVAMAIGKLYYDNEKWCWKGKPGVYTDYI 300
Db 241 YLHTAIVLTYSTDRLRKMFVICIGWGPVPIIIVAMAIGKLYYDNEKWCWKGKPGVYTDYI 300
QY 301 YQGPMILVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITTYMLFF 360
Db 301 YQGPMILVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITTYMLFF 360
QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
Db 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
QY 421 ARAWSIPTSPTRVSPHSIKOSTAV 444
Db 421 ARAWSIPTSPTRVSPHSIKOSTAV 444

RESULT 4
I38879
corticotropin releasing hormone receptor variant - human
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C/Accession: I38879
R/Ross, P.C.; Koetas, C.M.; Ramabhadran, T.V.
Biochem. Biophys. Res. Commun. 205, 1836-1842, 1994
A/Title: A variant of the human corticotropin-releasing factor (CRF) receptor: cloning, e
A/Reference number: I38879; MUID:95110332; PMID:7811272
A/Accession: I38879
A/Status: preliminary; translated from GB/EMBL/DBJ
```

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Db 332 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 391
QY 421 ARAWSIPTSPTRVSPHSIKOSTAV 444
Db 392 ARAWSIPTSPTRVSPHSIKOSTAV 415

RESULT 3
I58144
corticotropin-releasing factor receptor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: I58144
R/Chang, C.P.; Pearce, R.V.; O'Connell, S.; Rosenfeld, M.G.
Neuron 11, 1187-1195, 1993
A/Title: Identification of a seven transmembrane helix receptor for corticotropin-releas
A/Reference number: I58144; MUID:94099969; PMID:8274282
A/Accession: I58144
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-415 <RES>
A/Cross-references: UNIPROT:P35353; UNIPARC:UPI000002EF2A; GB:L25438; NID:g450298; PIDN:
C/Superfamily: glucagon receptor

Query Match 89.3%; Score 2126.5; DB 2; Length 415;
Best Local Similarity 90.8%; Pred. No. 5.6e-177; Indels 29; Gaps 1;
Matches 403; Conservative 5; Mismatches 7;

QY 1 MGGHPQLRLVKALLLGLNPNVSASLQDQCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
Db 1 MGRRPQLRLVKALLLGLNPNVSTSLQDQCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECEILNEEKSKKVHYHVAV 120
Db 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECEILNEEKSKKVHYHVAV 120
QY 121 IINVLGHICISLVALLVAFVFLRLRPGCTHWGQADGALVGPWVGAPQVRSIRCLR 180
Db 121 IINVLGHICISLVALLVAFVFLRLRPGCTHWGQADGALVGPWVGAPQVRSIRCLR 180
QY 181 NIIHWNLISAFILRNATFVQVLTMSPEVHQSNGVWCRLVTAAYNFHVTNPFPMFGEBC 240
Db 181 NIIHWNLISAFILRNATFVQVLTMSPEVHQSNGVWCRLVTAAYNFHVTNPFPMFGEBC 240
QY 241 YLHTAIVLTYSTDRLRKMFVICIGWGPVPIIIVAMAIGKLYYDNEKWCWKGKPGVYTDYI 300
Db 241 YLHTAIVLTYSTDRLRKMFVICIGWGPVPIIIVAMAIGKLYYDNEKWCWKGKPGVYTDYI 300
QY 301 YQGPMILVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITTYMLFF 360
Db 301 YQGPMILVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITTYMLFF 360
QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
Db 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
QY 421 ARAWSIPTSPTRVSPHSIKOSTAV 444
Db 392 ARAWSIPTSPTRVSPHSIKOSTAV 415

RESULT 4
I38879
corticotropin releasing hormone receptor variant - human
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C/Accession: I38879
R/Ross, P.C.; Koetas, C.M.; Ramabhadran, T.V.
Biochem. Biophys. Res. Commun. 205, 1836-1842, 1994
A/Title: A variant of the human corticotropin-releasing factor (CRF) receptor: cloning, e
A/Reference number: I38879; MUID:95110332; PMID:7811272
A/Accession: I38879
A/Status: preliminary; translated from GB/EMBL/DBJ
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A;Molecule type: mRNA
A;Residues: 1-375 <RES>
A;Cross-references: UNIPROT:P34998; UNIPARC:UPI000002A71E; EMBL:U16273; NID:9606973; PII
C;Superfamily: glucagon receptor

Query Match 80.9%; Score 1925.5; DB 2; Length 375;
Best Local Similarity 84.2%; Pred. No. 1.5e-159; Mismatches 1; Indels 69; Gaps 2;
Matches 374; Conservative 1

QY 1 MGGHPQLRLVKALLLGLNPVSASLODQHCHESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGGHPQLRLVKALLLGLNPVSASLODQHCHESLSLASNIS----- 40

QY 61 GQLVVRPCPAFFGVRYNTNNGYRECLANGSWAARVNYSECOEILNEEKSKVHYHAV 120
DB 41 -----DNGYRECLANGSWAARVNYSECOEILNEEKSKVHYHAV 80

QY 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWVGAPQVRRSIRCLR 180
DB 81 IINYLGHCHISLVALLVAFVFLRL-----RSIRCLR 111

QY 181 NIIHWNLSIAFILRNATWFFVQLTMSPEVHQSNGVWCRLVTAAYNFVHVTNPFWMFEGEC 240
DB 112 NIIHWNLSIAFILRNATWFFVQLTMSPEVHQSNGVWCRLVTAAYNFVHVTNPFWMFEGEC 171

QY 241 YLHTAIVLTVSTDRLRKRMFICIGWGVPPIIIVAWAIGKLYYDNEKWCWFGKRPQVTDYI 300
DB 172 YLHTAIVLTVSTDRLRKRMFICIGWGVPPIIIVAWAIGKLYYDNEKWCWFGKRPQVTDYI 231

QY 301 YQGPMLVLLINFIPIFNIRIILMTKLRASTTSETIYQKAVKATVLLPLLGITVYMLFP 360
DB 232 YQGPMLVLLINFIPIFNIRIILMTKLRASTTSETIYQKAVKATVLLPLLGITVYMLFP 291

QY 361 VNPGEDEVSRVVIYFNFSFLESQGFVSVFYCFNLSEVRSARIRKRWHRQDQKHSIRARV 420
DB 292 VNPGEDEVSRVVIYFNFSFLESQGFVSVFYCFNLSEVRSARIRKRWHRQDQKHSIRARV 351

QY 421 ARAMSIPTSPTRVSHSIKQSTAV 444
DB 352 ARAMSIPTSPTRVSHSIKQSTAV 375

RESULT 5
A55610
corticotropin-releasing factor receptor subtype 2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: A55610
R;Jovenberg, T.W.; Liaw, C.W.; Grigoriadis, D.B.; Clevenger, W.; Chalmers, D.T.; De Souza
Proc. Natl. Acad. Sci. U.S.A. 92, 836-840, 1995
A;Title: Cloning and characterization of a functionally distinct corticotropin-releasing
A;Reference number: A55610; MUID:95148632; PMID:7846062
A;Accession: A55610
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-411 <LOV>
A;Cross-references: UNIPROT:P47866; UNIPARC:UPI000012842E; EMBL:U16253; NID:9644771; PII
C;Genetics:
A;Gene: CRF2R
C;Superfamily: glucagon receptor

Query Match 65.1%; Score 1550.5; DB 2; Length 411;
Best Local Similarity 64.9%; Pred. No. 6.3e-127;
Matches 290; Conservative 59; Mismatches 52; Indels 53; Gaps 6;

QY 12 ALLLGLNPVSASLODQHCHESLSLASNI-----SGLQCNASVDLIGTCWPRS 58
DB 4 ALLL-----SLLEANC-SLALALLLDGGEPPDPGPGSYNCNTTILDOIGTCWPQS 54

QY 59 PAGQLVVRPCPAFFGVRYNTNNGYRECLANGSWAARVNYSECOEILNE-EKSKVHYH 117
DB 55 APGALVERPCPEYFNGIKYNTTRNAYRECLANGSWAARVNYSHCEPILDDKQRKYDLHYR 114

QY 118 VAVIINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWVGAPQVRRSIR 177
DB 115 IALIINYLGHCHISVVALVAALFLF-----VLRSSIR 145

QY 178 CLRNIIHWNLSIAFILRNATWFFVQLTMSPEVHQSNGVWCRLVTAAYNFVHVTNPFWMF 237
DB 146 CLRNIIHWNLSIAFILRNATWFFVQLTMSPEVHQSNGVWCRLVTAAYNFVHVTNPFWMF 204

QY 238 EGYLHTAIVLTVSTDRLRKRMFICIGWGVPPIIIVAWAIGKLYYDNEKWCWFGKRPQVYT 297
DB 205 EGYLHTAIVLTVSTDRLRKRMFICIGWGVPPIIIVAWAIGKLYYDNEKWCWFGKRPQVYT 264

QY 298 DYIQGPMLVLLINFIPIFNIRIILMTKLRASTTSETIYQKAVKATVLLPLLGITVY 357
DB 265 DYIQGPMLVLLINFIPIFNIRIILMTKLRASTTSETIYQKAVKATVLLPLLGITVY 324

QY 358 LFPVNPGEDEVSRVVIYFNFSFLESQGFVSVFYCFNLSEVRSARIRKRWHRQDQKHSIR 417
DB 325 LFPVNPGEDEVSRVVIYFNFSFLESQGFVSVFYCFNLSEVRSARIRKRWHRQDQKHSIR 384

QY 418 ARVARAMSIPTSPTRVSHSIKQSTAV 444
DB 385 VPVARAMSIPTSPTRVSHSIKQSTAV 411

RESULT 6
I49149
CRF receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49149
R;Ferrin, M.; Donaldson, C.; Chen, R.; Blount, A.; Berggren, T.; Bilezikjian, L.; Sawcher
Proc. Natl. Acad. Sci. U.S.A. 92, 2969-2973, 1995
A;Title: Identification of a second corticotropin-releasing factor receptor gene and char
A;Reference number: I49149; MUID:95224061; PMID:7708757
A;Accession: I49149
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-431 <RES>
A;Cross-references: UNIPROT:Q60748; UNIPARC:UPI0000028473; EMBL:U17858; NID:9727254; PII
C;Superfamily: glucagon receptor

Query Match 64.8%; Score 1543; DB 2; Length 431;
Best Local Similarity 62.4%; Pred. No. 3e-126;
Matches 287; Conservative 59; Mismatches 64; Indels 50; Gaps 7;

QY 2 GHPQLRLVKALLLGLNPVSA-----SLODQHCHESLSLASNISG--LQCN 45
DB 5 GSLPSAQLL--LCLFSLLPVLVQAQAPQDQPLMTLLEQYCHRTTI-GNFSGPTYTCN 61

QY 46 ASVDLIGTCWPRSPAGQLVVRPCPAFFGVRYNTNNGYRECLANGSWAARVNYSECOEI 105
DB 62 TTLDOIGTCWPQSAPGALVERPCPEYFNGIKYNTTRNAYRECLANGSWAARVNYSHCEPI 121

QY 106 LNE-EKSKVHYHVAIVINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAP 164
DB 122 LDDKQRKYDLHYRIALINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAP 159

QY 165 WSGAPQVRRSIRCLRNIHWNLSIAFILRNATWFFVQLTMSPEVHQSNGVWCRLVTAAY 224
DB 160 -----VLRSSIRCLRNIHWNLSIAFILRNATWFFVQLTMSPEVHQSNGVWCRLVTAAY 211

QY 225 NYFHTNPFWMFEGECYLHTAIVLTVSTDRLRKRMFICIGWGVPPIIIVAWAIGKLYYD 284
DB 212 NYFHTNPFWMFEGECYLHTAIVLTVSTDRLRKRMFICIGWGVPPIIIVAWAIGKLYY 271

QY 285 EKCFKGRPGVTDYIYQGPMLVLLINFIPIFNIRIILMTKLRASTTSETIYQKAVKA 344
DB 272 EKCFKGRPGVTDYIYQGPMLVLLINFIPIFNIRIILMTKLRASTTSETIYQKAVKA 331

QY 345 TLVLLPLLGITVYMLFFVNPGEDEVSRVVIYFNFSFLESQGFVSVFYCFNLSEVRSAR 404
DB 332 TLVLLPLLGITVYMLFFVNPGEDEVSRVVIYFNFSFLESQGFVSVFYCFNLSEVRSAR 391

Query Match	23.3%;	Score 554.5;	DB 2;	Length 593;
Best Local Similarity	31.6%;	Pred. No. 3.4e-40;	Indels 79;	Gaps 12;
Matches 131;	Conservative	58;	Mismatches 147;	

QY	37	SNISGLQCNASVDLIGTCWPRSPAGQVVRPCPAFFYGVRYNTNNGYRECLANGSW---	93
DB	101	SRYGRPCLPEWDHI-LCWPLGAPGEVAVPCPDYID--FNHKGHAYRCDRNGSWELV	157
QY	94	----AARVYSECOEILNEEKSKVHVHVAVINYLGHGICISLVALLVAFVLFLRLRPCT	149
DB	158	PGHNRTWANYSECVKFLTNETREREVFDRLGMIYTVGVYSVSLASTVA-VLIL-----	209
QY	150	HWGDQADGALGVGAPSGAPFQVRRSIRCLRNIIHWNLIISAFILRNATFWF-----	200
DB	210	-----AYF--RRLHCTRNYIHMHFLPSFMLRAVSIYFKDADVLSGA	248
QY	201	-----VQLTMSPEVHQSNVGMCRLLVTAANYFHTVTFMFMFGCGCYLHT	244
DB	249	TLDEAERLTEELRAIAQADPPATAAAGYAGCRVAVTFFLYFLATNYIWLVEGLYLS	308
QY	245	AVLVTYSTDRLRKWMFICIGWGPPIIIVAWAIGKLYYDNKECW--FGKRPVGVTDVIY	301
DB	309	LIFMAFFSEKKYLGWFTVFGWGLPAFVAVVSVRATLANTGCDLSSGNK-----KWII	363
QY	302	QGMILVLINFIENFIVRILMTKLR---ASTTSETIQYRKAVKATLVLLPLLGITYML	358
DB	364	QVILASIVLNFILINIVRLATKLRETNAGRCDTRQYRKLLKSTLVLMPLFGVHYI	423
QY	359	FFVNPGEDEVSRVVF---IVFNSFLSFQGFVSVFYCFNLSEVRSAIRKWHRW	410
DB	424	FMATP-YTEVSGTLWQVMHYEMLFNSFOGFVAILIYFCFCNGEYQAEIKKSWSRW	477

RESULT 11

S44203

parathyroid hormone-related peptide receptor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: S44203

R;Karperien, M.; van Dijk, T.B.; Hoelijmakers, T.; Cremers, F.; Abou-Samra, A.B. submitted to the EMBL Data Library, April 1994

A;Description: Expression pattern of parathyroid hormone/parathyroid hormone related protein in the mouse embryo

A;Reference number: S44203

A;Accession: S44203

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-591 <KAR>

A;Cross-references: UNIPROT:P41593; UNIPARC:UPI0000027984; EMBL:X78936; NID:947

C;Superfamily: Glucagon receptor

Query Match	22.8%;	Score 543.5;	DB 2;	Length 591;
Best Local Similarity	31.6%;	Pred. No. 3e-39;	Indels 73;	Gaps 13;
Matches 129;	Conservative	63;	Mismatches 143;	

QY	41	GLQCNASVDLIGTCWPRSPAGQVVRPCPAFFYGVRYNTNNGYRECLANGSW-----	93
DB	105	GRPCLPEWDNI-VCWPLGAPGEVAVPCPDYID--FNHKGHAYRCDRNGSWEVVPGHN	161
QY	94	AARVYSECOEILNEEKSKVHVHVAVINYLGHGICISLVALLVAFVLFLRLRPCTHWD	153
DB	162	RTWANYSECULKFMVNETREREVFDRLGMIYTVGVYSVSLASTVA-VLIL-----	209
QY	154	QADGALGVGAPSGAPFQVRRSIRCLRNIIHWNLIISAFILRNATFWVVLTM-----	205
DB	210	-----AYF--RRLHCTRNYIHMHFLPSFMLRAASIFVKDADVLSGFTLDE	252
QY	206	-----SPEVH-----QSNVGM--CRLVTAANYFHTVTFMFMFGCGCYLHTAIVL	248
DB	253	AERLTEBELHIIAQVPPPPAAAAGYAGCRVAVTFFLYFLATNYIWLVEGLYLSLIFM	312
QY	249	TYSTDLRLKWMFICIGWGPPIIIVAWAIGKLYYDNKECWFGKRPVGVTDVIYQGMILV	308

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QY 309 LLINFIPLFNIVRLMTKLR---ASTTSETIQYRKAVKATLVLLPLGLITMYLFFVNPGE 365
Db 371 VVLNFIPLFINIRVATKLRTHAGRCDDTRQYRKLLRSTLVLPVLFVGHVYTVFMALP-Y 429
QY 366 DEYSRVVVF---IYFNSFLESFQGFVSVFYCFNLSEVRSRAIRKRW 410
Db 430 TEVSGTLWQIMQHYEMLFNSFQGFVVAIIYFCNGEVAEIRKSWGRW 477

RESULT 12
154195
parathyroid hormone/parathyroid hormone related-peptide receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C/Accession: I54195; A42698
R:Pausova, Z.; Bourdon, J.; Clayton, D.; Mattei, M.G.; Seldin, M.F.; Janicic, N.; Rivier
Genomics 20, 20-26, 1994
A/Title: Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor
and rat genomes.
A/Reference number: I54195; MUID:94292182; PMID:8020952
A/Accession: I54195
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-591 <RES>
A/Cross-references: UNIPROT:P25961; UNIPARC:UPI00001329C2; GB:L19475; NID:G467316; PIDN:
R/Abou-Samra, A.B.; Juppner, H.; Forcè, T.; Freeman, M.W.; Kong, X.F.; Schipani, E.; Ure
Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1992
A/Title: Expression cloning of a common receptor for parathyroid hormone and parathyroid
n of both CAMP and inositol trisphosphates and increases intracellular free calcium.
A/Reference number: A42698; MUID:92212903; PMID:1313566
A/Accession: A42698
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-585, 'G', 587-591 <ABO>
A/Cross-references: UNIPARC:UPI00001789A7
A/Experimental source: ROS 17/2.8 osteosarcoma cells
A/Note: sequence extracted from NCBI backbone (NCBIP:92187)
C:Superfamily: glucagon receptor

Query Match 22.8%; Score 543.5; DB 2; Length 591;
Best Local Similarity 31.6%; Pred. No. 3e-39;
Matches 129; Conservative 63; Mismatches 143; Indels 73; Gaps 13;

QY 41 GLOQNASVDLIGTCWPSAPQGLVVRPCPAFFGVRYNTNNGYRECLANGSW----- 93
Db 105 GRPCLPEWDNI-VCMPLGAPGEVAVPCPDYID--FNHKGHAYRCDRNGSEVVPGHN 161
QY 94 AARVNYSECOEILNEEKKSVHYHVAIIIVNLGHCSLVALLVAFVLFLRLRPGCTHWGD 153
Db 162 RTWANYSECUKFTNTREREVEFDRLGMIYTVGSMSLASLTVA-VLIL----- 209
QY 154 QADGALEVGAPSGAPQVRRSIRCLRNIIHNLISAFILRNATFWVQLTM----- 205
Db 210 -----AYF---RRLHCTRNYIHMHFLSFMRLAASIFVKDAVLSGFTLDE 252
QY 206 -----SPEVH-----QSNVGH---CRLVTAANYFHVTFNFMFGECYLHAIVL 248
Db 253 AERLTEBELHIIAQVPPPPAAAAGVAGCRVAVTFPLYPLATNYYIWLVEGLYHLSIFM 312
QY 249 TGTDLRLKMMFICIGWGPFPPIIVAWAIGKLYYDNEKCFGRKPGVYTDYIYQGPMLIV 308
Db 313 AFPESEKKYLMGFTIFGWLGAFAVFAVWVGVRATLANTGCV--DLSSGHKKWIIQVPLAS 370
QY 309 LLINFIPLFNIVRLMTKLR---ASTTSETIQYRKAVKATLVLLPLGLITMYLFFVNPGE 365
Db 371 VVLNFIPLFINIRVATKLRTHAGRCDDTRQYRKLLRSTLVLPVLFVGHVYTVFMALP-Y 429
QY 366 DEYSRVVVF---IYFNSFLESFQGFVSVFYCFNLSEVRSRAIRKRW 410
Db 430 TEVSGTLWQIMQHYEMLFNSFQGFVVAIIYFCNGEVAEIRKSWGRW 477
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RESULT 13
JH0594
vasoactive intestinal peptide receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C/Accession: JH0594; S56014
R:Tshihara, T.; Shigemoto, R.; Mori, K.; Takahashi, K.; Nagata, S.
Neuron 8, 811-819, 1992
A/Title: Functional expression and tissue distribution of a novel receptor for vasoactive
A/Reference number: JH0594; MUID:92232309; PMID:1314625
A/Accession: JH0594
A/Molecule type: mRNA
A/Residues: 1-459 <ISH>
A/Cross-references: UNIPROT:P30083; UNIPARC:UPI0000055A96; GB:M86835; NID:G207640; PIDN:
R/Pei, L.; Meilmed, S.
Biochem. J. 308, 719-723, 1995
A/Title: Characterization of the rat vasoactive intestinal polypeptide receptor gene 5'
A/Reference number: S56014; MUID:97104266; PMID:8948424
A/Accession: S56014
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-26 <PEI>
A/Cross-references: UNIPARC:UPI00000053A; EMBL:U10635; NID:G505752; PIDN:AA848185.1; PII
C:Superfamily: glucagon receptor
C/Keywords: G protein-coupled receptor; glycoprotein; intestine; transmembrane protein
F:31-30/Domain: signal sequence #status predicted <SIG>
F:31-459/Product: vasoactive intestinal polypeptide receptor #status predicted <MAT>
F:146-168/Domain: transmembrane #status predicted <TM1>
F:176-195/Domain: transmembrane #status predicted <TM2>
F:218-241/Domain: transmembrane #status predicted <TM3>
F:256-277/Domain: transmembrane #status predicted <TM4>
F:295-318/Domain: transmembrane #status predicted <TM5>
F:344-363/Domain: transmembrane #status predicted <TM6>
F:376-395/Domain: transmembrane #status predicted <TM7>
F:58,69,100,292/Binding site: carbohydrate (Asn) #status predicted

Query Match 22.5%; Score 535; DB 2; Length 459;
Best Local Similarity 29.5%; Pred. No. 1.2e-38;
Matches 132; Conservative 80; Mismatches 149; Indels 86; Gaps 17;

QY 5 POLR---LVKALLLGLNPFV-SASLQDQH-CBSLSIASNISGLQCNASVDLIG----- 52
Db 7 PHVRMLCVLAGALCALRPAGQAASPOHECVLQI-EIQRCQCLEBAQLNETTGCCK 65
QY 53 -----TCWPRSPAGQLVVRPCPAFP-----YGVRYNTNNGYRECLANGSWAARVNY 99
Db 66 MWDNLTCWPTTPRQAVVLDCLIFQLFAPFIHGYNISRCTEBSWSQ-LEPGPYHIAAGL 124
QY 100 SECOEILNEEKKSVHYHVAIIIVNLGHCSLVALLVAFVLFLRLRPGCTHWGDQADGA 158
Db 125 NORASSLDEQQQTK--FYNTVKTGYTIGYSLASLLVAAI----- 164
QY 159 LEVGAPWSGAPQVRRSIRCLRNIIHNLISAFILRNATFWVQLTM--SPEV---HQS 213
Db 165 -----LSLFLKHLCTRNYIHMHFLSFMRLAATAVFIKDMALFNSGEIDHCSEAS 213
QY 214 VGCRLVTAANYFHVTFNFMFGECYLHAIVLTYSTDLRLKMMFICIGWGPFPPIIV 273
Db 214 VG-CKAAVVFFQYCVMANPFWLLVGLYLTLLAVSFPSERKYFWMGYILLGMGVPSPFIT 272
QY 274 AWAIGKLYYDNEKCFGRKPGVYTD-----YIYQGPMLIVLNLNPIFLFNIVRLMT 325
Db 273 ITWVRVIFDEGCV-----DTIINSSLWIIIPKAPILSILVNFIFCIIILVQ 323
QY 326 KLRASL--TSETIQYRKAVKATLVLLPLGLITMYLFFVNPGEDEVSVVFIYFNSFLESF 383
Db 324 KLRPPDIGKNDSSPYSRSLAKSTLLIPLFGIHYVMFAFP--DNFKAQKVMFELVVGSP 381
QY 384 QGFVSVFYCFNLSEVRSRAIRKRW 410
Db 382 QGFVVAIIYCFNLSEVRSRAIRKRW 408
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RESULT 14
I47130
calcitonin receptor-lb - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I47130
R;Zolnierowicz, S.; Cron, P.; Solinas-Toldo, S.; Fries, R.; Lin, H.Y.; Hemmings, B.A.
J. Biol. Chem. 269, 19530-19538, 1994
A;Title: Isolation, characterization, and chromosomal localization of the porcine calcitonin receptor
A;Reference number: A53972; MUID:94308241; PMID:8034723
A;Accession: I47130
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-498 <20>
A;Cross-references: UNIPROT:P25117; UNIPARC:UPI0000126E78; EMBL:Z31356; NID:9531126; PII
C;Genetics:
A;Introns: 17/3; 70/1; 107/1; 144/3; 175/2; 233/3; 285/1; 305/2; 327/3; 400/3; 414/3
C;Superfamily: glucagon receptor

Query Match 22.4%; Score 533; DB 2; Length 498;
Best Local Similarity 32.0%; Pred. No. 2e-38;
Matches 129; Conservative 84; Mismatches 142; Indels 48; Gaps 15;

QY 41 GLOCNASVDLIG-TCTPRSPAGQIVRPPCPAPP--YGRVNTT-----NNGYRECLANG 91
DB 70 GLYCNRTWD--GWSWDDTDPAGVLAECYCPDYPDPDAEKVKYKCGEDGDWYRHPSNI 127
QY 92 SWAARNVYSECQELNEE-KKSKVHYHVAIIVNLYGHCISLVALLVAFVFLRLRPGCTH 150
DB 128 SWS---NYTWCAFTPKQNAVILYLAIV---GHSLSITLLISLGIFMELR----- 175
QY 151 WGDQADGALEVGAPWSGAPPQVRISIRCLRNIIHWNLSAFILRNATFWVVOQLTM---SP 207
DB 176 -----YFNLLAPPENALLYPT-RSISQVRVTLHKMFLTYVL-NSIIIVHLVWVTPNG 226
QY 208 EVHQSNVGVCRLYTAAYNYFHVTFNFMFGEGCVLHTAIVLTYSTDLRKWMFICIGWGV 267
DB 227 ELVKRDPPICKVLHFFHQYMNCSNYFMMLCEGYLHTLIIVSVFAEQRLMWHYVLGWF 286
QY 268 PPPIIWAVALGLYDNEKCFGRPGVYTD--YIYQGPMLVLLINFIENIVRLMT 325
DB 287 PLIPTTAHATRAVLFDNDCWL-----SVDNLLYIIGHVPVMAALVNVFFLLILRLVLK 342
QY 326 KLRASSTSETIQYRKAVKATLVLLPLLGITYMLFFVNPGEDEVSRVVFYIFNSFLESFQG 385
DB 343 KLESQEAESHMYLKAVRATLILVPLLGQVQVPLPWRPSTPLLGK-IYDYVHSLIHFG 401
QY 386 FFVSFYCFPLNSVRSAIRKRWH-----RWODKHSIRARVARA 423
DB 402 FFVAIIYFCNHEVOGALKRQWQYQQRWAGRRSTRANAAAA 444

RESULT 15
S16319
secretin receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S16319
R;Ishihara, T.; Nakamura, S.; Kaziro, Y.; Takahashi, T.; Takahashi, K.; Negata, S.
EMBO J. 10, 1635-1641, 1991
A;Title: Molecular cloning and expression of a cDNA encoding the secretin receptor.
A;Reference number: S16319; MUID:91266890; PMID:1646711
A;Accession: S16319
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-449 <1SH>
A;Cross-references: UNIPROT:P23811; UNIPARC:UPI000013569A; EMBL:X59132; NID:957228; PII
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 22.3%; Score 531.5; DB 2; Length 449;
Best Local Similarity 31.7%; Pred. No. 2.5e-38;

Matches 152; Conservative 64; Mismatches 154; Indels 109; Gaps 20;

QY 7 LRLVKALLLLGNP-----VSASLQDQ--HC-BELS-----IASNISGLQCHASVD 49
DB 17 LLLTKAHTVGVPPRLCDVRRVLLERAHCLQQLSKKKGALGPETASGCEGLWNNMS-- 74
QY 50 LIGTCWPRSPAGQIVRPPCPAPPY-----GVRYNTTNGYRECLANGSWAARVNYSEC 102
DB 75 -----CWPSAPARTVEVCQPKFLMLSNKNGSLFRNCTQDGWSETPRPDLAGCVNINS 130
QY 103 QEILNEEK-----KSKVHYHVAIIVNLYGHCISLVALLVAFVFLRLRPGCTHMGDQADG 157
DB 131 ---FNERRHAYLLKLVMTV-----GVSSSLAMLLVALSIL-----CSF----- 167
QY 158 ALEVGAWSGAPPQVRISIRCLRNIIHWNLSAFILRNATFWV--VOLTMSPEV-----HQS 212
DB 168 -----RRLHCTRNTHMHLFVSVFILRLALSNTFKDAVLFSSDDVVTYCDAH 211
QY 213 NVGWCCLVTAAYNYFHVTFNFMFGEGCVLHTAIVLTYSTDLRKWMFICIGWGVPPPII 272
DB 212 KVG-CKLVMIFFQYCIIMANYAMLLVEGLYLLTLAISFFSERKYLOAFVLGWSGSPAIFV 270
QY 273 VAWAIGKLYDNEKWC-FGRKPGVYTDYIYQGPMLVLLINFIENIVRLMTKLRAS 331
DB 271 ALWATRHFLENTGCGWDINANASVW--WIRGVPVILSILINFIENILRLMKLRTOE 328
QY 332 T--SETIQYRKAVKATLVLLPLLGITYMLFFVNPGEDEVSRVVFYIFNSFLESFQGPFVS 389
DB 329 TRGSETNHYKRLAKSTLLIPLFGIHHVIVFAFSP-EDAME--VOLFFELALGSFQGLVWA 385
QY 390 VFYCFPLNSVRSAIRKRWHQ-----DKHSIRARVARAMSIP 427
DB 386 VLYCFPLNGEVOLEVOQKRWQHLQEPFLRPVAFNFSFNATNGPTHTSKASTQSRISIP 444

Search completed: March 16, 2006, 17:21:00
Job time : 43 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: March 16, 2006, 17:13:03 ; Search time 231 Seconds
(without alignments)
1356.080 Million cell updates/sec
Title: US-10-649-193-15
Perfect score: 2381
Sequence: 1 MGHQPQLRVKALLGLNP.....SIPTSPTRVFSIKQSTAV 444

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2381	100.0	444	1 CRFRI_HUMAN	P34998 homo sapien
2	2324	97.6	447	2 CRNG71_HUMAN	Q8ng71 homo sapien
3	2186.5	91.8	415	2 Q4QRJ1_HUMAN	Q4qrj1 macaca mulle
4	2172.5	91.2	415	2 Q76L18_MACMU	Q76l18 macaca mulle
5	2146.5	90.2	415	2 Q8WMM0_TUPGB	Q8wm00 tupai glis
6	2137.5	89.8	415	1 CRFRI_MOUSE	P35347 mus musculus
7	2128.5	89.4	415	2 Q8K3R2_MESAU	Q8k3r2 mesocricetu
8	2126.5	89.3	415	1 CRFRI_RAT	P35353 rattus norv
9	2126.5	89.3	415	2 Q9BGU4_BOVIN	Q9bgua bos taurus
10	2086.5	87.6	415	1 CRFRI_SHEEP	O62772 ovis aries
11	1945	81.7	420	1 CRFRI_CHICK	Q90812 gallus gall
12	1817.5	76.3	445	2 Q98UC2_9TELE	Q98uc2 ameaurus ne
13	1804	75.8	430	2 Q8AWA2_ONCKE	Q8aw2a oncorhynch
14	1796.5	75.5	415	1 CRFRI_XENLA	O42602 xenopus lae
15	1789	75.1	416	2 Q8YV61_RANCA	Q8yv61 rana catesb
16	1765	74.1	434	2 Q7T3S9_FUGRU	Q7t3s9 fugu rubrip
17	1741.5	73.1	428	2 Q98UC0_9TELE	Q98uc0 ameaurus ne
18	1676.5	70.4	315	2 Q4JHT0_CERAE	Q4jht0 ceratopithe
19	1631	68.5	365	2 Q5GH80_ONCMY	Q5gh80 oncorhynch
20	1617.5	67.9	329	2 Q70JV6_CYPCA	Q70jv6 cyprinus ca
21	1603.5	67.3	412	2 Q7Z2Z2_CHICK	Q7z2z2 gallus gall
22	1580	66.4	437	2 Q8WML8_TUPGB	Q8wml8 tupai glis
23	1576.5	66.2	414	2 Q8AWA1_ONCKE	Q8aw1 oncorhynch
24	1561	65.6	405	2 Q98UC1_9TELE	Q98uc1 ameaurus ne
25	1559	65.5	410	2 Q8WML9_TUPGB	Q8wml9 tupai glis
26	1550.5	65.1	411	1 CRFRI_RAT	P47866 rattus norv
27	1549.5	65.1	411	1 CRFRI_HUMAN	Q13324 homo sapien
28	1549.5	65.1	411	2 Q4QRJ4_HUMAN	Q4qrj4 homo sapien
29	1543	64.8	431	1 CRFRI_MOUSE	Q60748 mus musculus
30	1541.5	64.7	413	1 CRFRI_XENLA	O42603 xenopus lae
31	1530.5	64.3	411	2 Q5GL24_MOUSE	Q5gl24 mus musculus

32	1515.5	63.6	411	2 Q68Y60_RANCA	Q68yv60 rana catesb
33	1429	60.0	501	2 Q4S8L0_TETNG	Q4s8l0 tetraodon n
34	949	39.9	186	2 Q5PY21_EPICO	Q5py21 epinephelus
35	743.5	31.2	277	2 Q8BJD9_MOUSE	Q8bjd9 m mus muscu
36	732.5	30.8	153	2 Q95L49_BOVIN	Q95l49 bos taurus
37	703	29.5	441	1 Q1HR_ACHDO	Q1hr983 acheta dome
38	686	28.8	150	2 Q5J877_ONCMY	Q5j877 oncorhynch
39	663.5	27.9	154	2 Q7TSA2_MESAU	Q7tsa2 mesocricetu
40	663	27.8	475	2 Q4V3E9_DROME	Q4v3e9 drosophila
41	662.5	27.8	454	2 Q7Q773_ANOGA	Q7q773 anopheles g
42	662.5	27.8	504	2 Q9V716_DROME	Q9v716 drosophila
43	651.5	27.4	388	2 Q9V6C7_DROME	Q9v6c7 drosophila
44	638	26.8	641	2 Q65AS2_9HEMI	Q65as2 nilaparvata
45	635	26.7	631	2 Q65AS3_9HEMI	Q65as3 nilaparvata

ALIGNMENTS

RESULT 1
ID CRFRI_HUMAN STANDARD; PRT; 444 AA.
AC P34998; Q13008; Q9UK64;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)
DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).
GN Name=CRHR1; Synonyms=CRFR, CRFRI, CRHR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS CRF-R1 AND CRF-R2).
RC TISSUE=Pituitary; PubMed=7692441;
RX MEDLINE=94022296; PubMed=7692441; Vale W.M.;
RA Chen R., Lewis K.A., Perrin M.H., Vale W.M.;
RT "Expression cloning of a human corticotropin-releasing-factor
receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8967-8971(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM CRF-R2).
RC TISSUE=Brain;
RX MEDLINE=94063063; PubMed=8243652; DOI=10.1016/0014-5793(93)80427-V;
RA Vita N., Laurent P., Lefort S., Chalon P., Lelias J.-M., Kaghad M.,
le Fur G., Caput D., Ferrara P.;
RT "Primary structure and functional expression of mouse pituitary and
human brain corticotropin releasing factor receptors.";
RL FEBS Lett. 335:1-5(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=98434445; PubMed=9757017; DOI=10.1016/S0378-1119(98)00322-9;
RA Sakai K., Yamada M., Horiba N., Wakui M., Demura H., Suda T.;
RT "The genomic organization of the human corticotropin-releasing factor
type-1 receptor.";
RL Gene 219:125-130(1998).
RN [4]
RP NUCLEOTIDE SEQUENCE (ISOFORM CRF-R3).
RC TISSUE=Hippocampus;
RX MEDLINE=95110332; PubMed=7811272;
RA Ross P.C., Koskas C.M., Ramabhadran T.V.;
RT "A variant of the human corticotropin-releasing factor (CRF) receptor:
cloning, expression and pharmacology.";
RL Biochem. Biophys. Res. Commun. 205:1836-1842(1994).
RN [5]
RP NUCLEOTIDE SEQUENCE (ISOFORM CRF-R4).
RX MEDLINE=20065650; PubMed=10598591; DOI=10.1210/me.13.12.2189;
RA Grammatopoulos D.K., Dai Y., Randeve H.S., Levine M.A., Karteris E.,
Easton A.J., Hillhouse E.W.;
RT "A novel spliced variant of the type 1 corticotropin-releasing hormone
receptor with a deletion in the seventh transmembrane domain present

RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC096836; AAH96836.1; -, mRNA.
 KW Receptor.
 SQ SEQUENCE 415 AA; 47671 MW; 81445283CCB34C6E CRC64;

Query Match 91.8%; Score 2186.5; DB 2; Length 415;
 Best Local Similarity 93.5%; Pred. No. 4.7e-173;
 Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY 1 MGGHPQLRLVKALLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
 DB 1 MGGHPQLRLVKALLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
 QY 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQIILNEEKSKVHYHVA 120
 DB 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQIILNEEKSKVHYHVA 120
 QY 121 IINYLGHCSLVALLVAFVFLRLPGCTHMGDQADGALEVGAPWPGAPFQVRRSIRCLR 180
 DB 121 IINYLGHCSLVALLVAFVFLRL-----RSIRCLR 151
 QY 181 NIHNWNLISAFILRNATFVQVLTMSPEVHQSNGVWCRLVTAAYNYFHVTFNPFMFGECC 240
 DB 152 NIHNWNLISAFILRNATFVQVLTMSPEVHQSNGVWCRLVTAAYNYFHVTFNPFMFGECC 211
 QY 241 YLHTAIVLTYSTDLRKWMPICIGWGPVPIIIVAWAIGKLYDNEKWCWPKRGVVTDYI 300
 DB 212 YLHTAIVLTYSTDLRKWMPICIGWGPVPIIIVAWAIGKLYDNEKWCWPKRGVVTDYI 271
 QY 301 YQGPMLVLLINFIPLNFIVRLMTKLRASTTSETIOYRKAVKATVLLPLLGITYMLFF 360
 DB 272 YQGPMLVLLINFIPLNFIVRLMTKLRASTTSETIOYRKAVKATVLLPLLGITYMLFF 331
 QY 361 VNPGEDEVSRVFIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRQDGHSTRARV 420
 DB 332 VNPGEDEVSRVFIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRQDGHSTRARV 391
 QY 421 ARAMSIPSTPTVRSFHSIKQSTAV 444
 DB 392 ARAMSIPSTPTVRSFHSIKQSTAV 415

RESULT 4

Q76LL8 MACMU
 ID Q76LL8_MACMU PRELIMINARY; PRT; 415 AA.
 AC Q76LL8,
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Corticotropin releasing factor receptor type 1.
 GN Name=CRF1;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopitheciidae; Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Ohida Y., Ikeda Y., Chaki S., Okuyama S.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB078141; BAD02831.1; -, mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004930; P:G-protein coupled receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR003052; CRF1 receptor.
 DR InterPro; IPR003051; CRF receptor.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR01279; CRFRECEPTOR.

DR PRINTS; PR01280; CRFRECEPTOR1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
 KW Receptor.
 SQ SEQUENCE 415 AA; 47784 MW; 84C530DEC6DA97AD CRC64;

Query Match 91.2%; Score 2172.5; DB 2; Length 415;
 Best Local Similarity 93.0%; Pred. No. 6.9e-172;
 Matches 413; Conservative 0; Mismatches 2; Indels 29; Gaps 1;

QY 1 MGGHPQLRLVKALLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
 DB 1 MGGHPQLRLVKALLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
 QY 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQIILNEEKSKVHYHVA 120
 DB 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQIILNEEKSKVHYHVA 120
 QY 121 IINYLGHCSLVALLVAFVFLRLPGCTHMGDQADGALEVGAPWPGAPFQVRRSIRCLR 180
 DB 121 IINYLGHCSLVALLVAFVFLRL-----RSIRCLR 151
 QY 181 NIHNWNLISAFILRNATFVQVLTMSPEVHQSNGVWCRLVTAAYNYFHVTFNPFMFGECC 240
 DB 152 NIHNWNLISAFILRNATFVQVLTMSPEVHQSNGVWCRLVTAAYNYFHVTFNPFMFGECC 211
 QY 241 YLHTAIVLTYSTDLRKWMPICIGWGPVPIIIVAWAIGKLYDNEKWCWPKRGVVTDYI 300
 DB 212 YLHTAIVLTYSTDLRKWMPICIGWGPVPIIIVAWAIGKLYDNEKWCWPKRGVVTDYI 271
 QY 301 YQGPMLVLLINFIPLNFIVRLMTKLRASTTSETIOYRKAVKATVLLPLLGITYMLFF 360
 DB 272 YQGPMLVLLINFIPLNFIVRLMTKLRASTTSETIOYRKAVKATVLLPLLGITYMLFF 331
 QY 361 VNPGEDEVSRVFIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRQDGHSTRARV 420
 DB 332 VNPGEDEVSRVFIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRQDGHSTRARV 391
 QY 421 ARAMSIPSTPTVRSFHSIKQSTAV 444
 DB 392 ARAMSIPSTPTVRSFHSIKQSTAV 415

RESULT 5

Q8WMM0 TUPGB
 ID Q8WMM0_TUPGB PRELIMINARY; PRT; 415 AA.
 AC Q8WMM0,
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Corticotropin releasing factor type 1 receptor.
 GN Name=crf1;
 OS Tupiaia glis belangeri (Common tree shrew).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Scandentia; Tupaiidae; Tupiaia.
 OX NCBI_TaxID=37347;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=99067019; PubMed=9851694;
 RX Falchaudhuri M.R., Wille S., Mevenkamp G., Spiess J., Fuchs E.,
 RA Bautzenberg F.M.;
 RT "Corticotropin-releasing factor receptor type 1 from Tupiaia belangeri:
 RT cloning, functional expression and tissue distribution.";
 RL Eur. J. Biochem. 258:78-84(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Bautzenberg F.M.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ422241; CAD19577.1; -, mRNA.

DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0016020; C: membrane; IEA.
 DR GO: GO:0004930; P: G-protein coupled receptor activity; IEA.
 DR GO: GO:0004872; P: receptor activity; IEA.
 DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . ; IEA.
 DR InterPro: IPR003052; CRF1 receptor.
 DR InterPro: IPR003051; CRF1 receptor.
 DR InterPro: IPR000832; GPCR secretin.
 DR InterPro: IPR001879; hormn_receptor.
 DR Pfam: PF00002; 7tm_2; 1.
 DR Pfam: PF02793; HRM; 1.
 DR PRINTS; PR01279; CRFRECEPTOR.
 DR PRINTS; PR01280; CRFRECEPTOR.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
 KW Receptor.
 SQ SEQUENCE 415 AA; 47685 MW; 97B9ABE050AC08D CRC64;
 Query Match 90.2%; Score 2146.5; DB 2; Length 415;
 Best Local Similarity 91.7%; Pred. No. 1e-169;
 Matches 407; Conservative 3; Mismatches 5; Indels 29; Gaps 1;
 QY 1 MGGHPQLRLVKALLGLNLPVSLAQDQHCESLSLASNTISGLQCNASVDLIGTCWPRSPA 60
 DB 1 MGRGPHRLRLVKALLGLNLPVSLAQDQHCESLSPTSNSVGLQCNASVDLIGTCWPRSPA 60
 QY 61 GQLVVRPCAPFYGVRYNTNNGYRECLANGSWAARVNSCEILNEEKSKVHHVAV 120
 DB 61 GQLVVRPCAPFYGVRYNTNNGYRECLANGSWAARVNSCEILNEEKSKVHHVAV 120
 QY 121 IINYLGHCSLVALLVAFVFLRLRPOCTHWGQADGALVGPWSPAPQVRRSIRCLR 180
 DB 121 IINYLGHCSLVALLVAFVFLRLR-----RSIRCLR 151
 QY 181 NIHWNLISAFILRNATFVYVQLTMSPEVHQSNVGCRLVTAAYNPVHTNFFWFGEGC 240
 DB 152 NIHWNLISAFILRNATFVYVQLTMSPEVHQSNVGCRLVTAAYNPVHTNFFWFGEGC 211
 QY 241 YLHTAIVLTSTDLRLKWMFICIGWVPFPIIIVAWAIGKLYYNEKCFGRFGVTDYI 300
 DB 212 YLHTAIVLTSTDLRLKWMFVCIWGVPPFPIIIVAWAIGKLYYNEKCFGRFGVTDYI 271
 QY 301 YQGPMLVLLINFIENFNLVIRILMTKLRASTTSTIQYKAVKATLVLLPLLGITYMLFF 360
 DB 272 YQGPMLVLLINFIENFNLVIRILMTKLRASTTSTIQYKAVKATLVLLPLLGITYMLFF 331
 QY 361 VNPGEDEVSRVFIYFNFSFLESFGQFPVSVFYCFNLSEVRSALKRWHRWQDXHSIRARV 420
 DB 332 VNPGEDEVSRVFIYFNFSFLESFGQFPVSVFYCFNLSEVRSALKRWHRWQDXHSIRARV 391
 QY 421 ARAMSIPTSPTRVSHSIKOSTAV 444
 DB 392 ARAMSIPTSPTRVSHSIKOSTAV 415

RESULT 6

CRFR1 MOUSE
 ID CRFR1 MOUSE STANDARD; PRT; 415 AA.
 AC P35347;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)
 DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).
 GN Name=Crhr1; Synonyms=Crhr;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE= pituitary;
 RX MEDLINE=94063063; PubMed=8243652; DOI=10.1016/0014-5793(93)80427-V;
 RA Vita N., Laurent P., Lefort S., Chalon P., Lelias J.-M., Kaghad M.,
 le Fur G., Caput D., Ferrara P.;
 RT "Primary structure and functional expression of mouse pituitary and
 human brain corticotrophin releasing factor receptors.";
 RL FEBS Lett. 335:1-5(1993).
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ILS, and ISS;
 RX MEDLINE=21363810; PubMed=11471062; DOI=10.1007/s00335-001-1001-x;
 RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Caniff J.,
 Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
 RT "High-throughput sequence identification of gene coding variants
 within alcohol-related QTLs.";
 RL Mamm. Genome 12:657-663(2001).
 CC -1- FUNCTION: This is a receptor for corticotropin releasing factor.
 CC Shows high-affinity CRF binding. The activity of this receptor is
 mediated by G proteins which activate adenylyl cyclase.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC TISSUE SPECIFICITY: Brain, pituitary gland, testis. Not detected
 CC in placenta, peripheral blood, lymphocytes, kidney and liver.
 CC -1- PTM: Carboxyl-terminal Ser or Thr residues may be phosphorylated.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC ENBL; X72305; CAA51053.1; -; mRNA.
 DR ENBL; A483484; AAL90758.1; -; mRNA.
 DR ENBL; A483485; AAL90759.1; -; mRNA.
 DR PIR; S39535; S39535.
 DR Ensembl; ENSMUSG0000018634; Mus musculus.
 DR MGI; MGI:88498; Crhr1.
 DR GO: GO:0005615; C: extracellular space; TAS.
 DR GO: GO:0016021; C: integral to membrane; TAS.
 DR GO: GO:0015056; P: corticotropin-releasing factor receptor ac. . ; IMP.
 DR GO: GO:0007610; P: behavior; IMP.
 DR GO: GO:0006950; P: response to stress; IMP.
 DR InterPro: IPR003052; CRF1 receptor.
 DR InterPro: IPR003051; CRF1 receptor.
 DR InterPro: IPR000832; GPCR secretin.
 DR InterPro: IPR001879; hormn_receptor.
 DR PANTHER; PTHR1011:SF16; CRF_receptor; 1.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR01279; CRFRECEPTOR.
 DR PRINTS; PR01280; CRFRECEPTOR.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
 KW G-protein coupled receptor; Glycoprotein; Phosphorylation; Receptor;
 KW Signal; Transducer; Transmembrane.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 415 Corticotropin releasing factor receptor
 FT FT 1.
 FT TOPO_DOM 24 121 Extracellular (Potential).
 FT TRANSMEM 122 142 1 (Potential).
 FT FT TOPO_DOM 143 151 Cytoplasmic (Potential).
 FT TRANSMEM 152 171 2 (Potential).
 FT FT TOPO_DOM 172 189 Extracellular (Potential).
 FT TRANSMEM 190 213 3 (Potential).
 FT FT TOPO_DOM 214 227 Cytoplasmic (Potential).
 FT TRANSMEM 228 249 4 (Potential).

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FT TOPO_DOM 250 268 Extracellular (Potential).
FT TRANSMEM 269 291 5 (Potential).
FT TOPO_DOM 292 314 Cytoplasmic (Potential).
FT TRANSMEM 315 334 6 (Potential).
FT TOPO_DOM 335 349 Extracellular (Potential).
FT TRANSMEM 350 369 7 (Potential).
FT TOPO_DOM 370 415 Cytoplasmic (Potential).
FT CARBOHYD 38 38 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 45 45 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 78 78 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).
FT DISULFID 98 98 N-linked (GlcNAc...) (Potential).
FT DISULFID 30 54 By similarity.
FT DISULFID 44 87 By similarity.
FT DISULFID 68 102 By similarity.
SQ SEQUENCE 415 AA; 47769 MW; 81433BDA6D1CA070 CRC64;

Query Match 89.8%; Score 2137.5; DB 1; Length 415;
Best Local Similarity 91.2%; Pred. No. 5.6e-169;
Matches 405; Conservative 4; Mismatches 6; Indels 29; Gaps 1;

QY 1 MGHPQLRLVKALLLLGLNPVSASLDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGQRPLRLVKALLLLGLNPVSTSLDQHCESLSLASNVSGLQCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNTYSECOEILNEEKSKVHYHVAV 120
DB 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNTYSECOEILNEEKSKVHYHVAV 120
QY 121 IINYLGHGISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWMSGAPFQVRRSIRCLR 180
DB 121 IINYLGHGISLVALLVAFVFLRLR-----RSIRCLR 151
QY 181 NIHNWNLISAFILRNATWFWVQVTMSPEVHQSNVGCRLVTAAYNFHVTFNPFMFGECC 240
DB 152 NIHNWNLISAFILRNATWFWVQVTSPVHQSNVAVCRLVTAAYNFHVTFNPFMFGECC 211
QY 241 YLHTAIVLTYSTDLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKWCWKGKRGVVDYI 300
DB 212 YLHTAIVLTYSTDLRKWMFVCIWGVPPPIIVAMAIGKLYYDNEKWCWKGKRGVVDYI 271
QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETTIQYRKAVKATLVLLPLLGITYMLFF 360
DB 272 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETTIQYRKAVKATLVLLPLLGITYMLFF 331
QY 361 VNPGEDEVSRVFIYFNSFLESQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVFIYFNSFLESQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSPHSIKQSTAV 444
DB 392 ARAMSIPTSPTRVSPHSIKQSTAV 415

RESULT 7
Q8K3R2_MESAU PRELIMINARY; PRT; 415 AA.
AC Q8K3R2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Type-1 corticotropin-releasing hormone receptor alpha isoform.
GN Name-CRH-R1;
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetinae; Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Piszczak A.V., Slominski A.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY034599; AAK59707.1; -, mRNA.

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DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR003052; CRF1_receptor.
DR InterPro; IPR000832; GPCR_receptor.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR01279; CRPRECEPTOR.
DR PRINTS; PR01280; CRPRECEPTOR1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormb_1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00327; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 415 AA; 47702 MW; 500B4DD617E5F19E CRC64;

Query Match 89.4%; Score 2128.5; DB 2; Length 415;
Best Local Similarity 90.8%; Pred. No. 3.1e-168;
Matches 403; Conservative 5; Mismatches 7; Indels 29; Gaps 1;

QY 1 MGHPQLRLVKALLLLGLNPVSASLDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGQRPLRLVKALLLLGLNPVSTSLDQHCESLSLASNVSGPQCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNTYSECOEILNEEKSKVHYHVAV 120
DB 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNTYSECOEILNEEKSKVHYHVAV 120
QY 121 IINYLGHGISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWMSGAPFQVRRSIRCLR 180
DB 121 IINYLGHGISLVALLVAFVFLRLR-----RSIRCLR 151
QY 181 NIHNWNLISAFILRNATWFWVQVTMSPEVHQSNVGCRLVTAAYNFHVTFNPFMFGECC 240
DB 152 NIHNWNLISAFILRNATWFWVQVTMSPEVHQSNVGCRLVTAAYNFHVTFNPFMFGECC 211
QY 241 YLHTAIVLTYSTDLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKWCWKGKRGVVDYI 300
DB 212 YLHTAIVLTYSTDLRKWMFVCIWGVPPPIIVAMAIGKLYYDNEKWCWKGKRGVVDYI 271
QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETTIQYRKAVKATLVLLPLLGITYMLFF 360
DB 272 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETTIQYRKAVKATLVLLPLLGITYMLFF 331
QY 361 VNPGEDEVSRVFIYFNSFLESQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVFIYFNSFLESQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSPHSIKQSTAV 444
DB 392 ARAMSIPTSPTRVSPHSIKQATAV 415

RESULT 8
CRFR1_RAT
ID CRFR1_RAT STANDARD; PRT; 415 AA.
AC P35353;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)
DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).
GN Name-Crhrl; Synonyms-Crhrl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.

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OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=94062694; PubMed=8243336; DOI=10.1210/en.133.6.3059;
RA Perrin M.H., Donaldson C.J., Chen R., Lewis K.A., Vale W.W.;
RT "Cloning and functional expression of a rat brain corticotropin
releasing factor (CRF) receptor.";
RL Endocrinology 133:3058-3061(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=9409969; PubMed=8274282; DOI=10.1016/0896-6273(93)90230-O;
RA Chang C.P., Pearce R.V. II, O'Connell S., Rosenfeld M.G.;
RT "Identification of a seven transmembrane helix receptor for
corticotropin-releasing factor and sauvagine in mammalian brain.";
RL Neuron 11:1187-1195(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=testis;
RX MEDLINE=96278921; PubMed=8662941; DOI=10.1074/jbc.271.24.14519;
RA Tsai-Morris C.-H., Buczeko E., Geng Y., Gamboa-Pinto A., Dufau M.L.;
RT "The genomic structure of the rat corticotropin releasing factor
receptor. A member of the class II G protein-coupled receptors.";
RL J. Biol. Chem. 271:14519-14525(1996).
RN [4]
RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=21451158; PubMed=11567096; DOI=10.1110/ps.12101;
RA Hofmann B.A., Sydow S., Jahn O., van Werven L., Liepold T., Eckart K.,
Spies J.;
RT "Functional and protein chemical characterization of the N-terminal
domain of the rat corticotropin-releasing factor receptor 1.";
RL Protein Sci. 10:2050-2062(2001).
CC -I- FUNCTION: This is a receptor for corticotropin releasing factor.
CC Shows high-affinity CRF binding. The activity of this receptor is
mediated by G proteins which activate adenylyl cyclase.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: Entire nervous system.
CC -I- PTM: Carboxyl-terminal Ser or Thr residues may be phosphorylated.
CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
CC
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
CC EMBL; L24096; -; NOT ANNOTATED CDS; mRNA.
CC EMBL; L25438; AAAL6441.1; -; Genomic DNA.
CC EMBL; US3498; AAC3519.1; -; Genomic DNA.
CC EMBL; US3486; AAC3519.1; JOINED; Genomic DNA.
CC EMBL; US3487; AAC3519.1; JOINED; Genomic DNA.
CC EMBL; US3488; AAC3519.1; JOINED; Genomic DNA.
CC EMBL; US3489; AAC3519.1; JOINED; Genomic DNA.
CC EMBL; US3490; AAC3519.1; JOINED; Genomic DNA.
CC EMBL; US3491; AAC3519.1; JOINED; Genomic DNA.
CC EMBL; US3492; AAC3519.1; JOINED; Genomic DNA.
CC EMBL; US3493; AAC3519.1; JOINED; Genomic DNA.
CC EMBL; US3494; AAC3519.1; JOINED; Genomic DNA.
CC EMBL; US3495; AAC3519.1; JOINED; Genomic DNA.
CC EMBL; US3496; AAC3519.1; JOINED; Genomic DNA.
CC EMBL; US3497; AAC3519.1; JOINED; Genomic DNA.
CC F01; I58144; I58144.
CC Ensembl; ENSRNOG0000004900; Rattus norvegicus.
CC RGD; 61376; Crhl.
CC GO; GO:0004930; F-G-protein coupled receptor activity; IDA.
CC GO; GO:0007188; P-G-protein signaling, coupled to cAMP nucleo. .; IDA.
CC GO; GO:0007218; P-neuropeptide signaling pathway; IDA.
CC InterPro; IPR003052; CRF1 receptor.
CC InterPro; IPR003051; CRF receptor.
CC InterPro; IPR000832; GPCR_secretin.
CC InterPro; IPR001879; hormn_receptor.
CC PANTHER; PTHR12011:SF16; CRF_receptor; 1.

DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PRO1279; CRFRECEPTOR.
DR PRINTS; PRO1280; CRFRECEPTOR1.
DR PRINTS; PRO0249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
KW G-protein coupled receptor; Glycoprotein; Phosphorylation; Receptor;
KW Signal; Transducer; Transmembrane.
FT SIGNAL 1 23
FT CHAIN 24 415
FT -----
FT TOPO_DOM 24 121
FT TRANSMEM 122 142
FT TOPO_DOM 143 151
FT TRANSMEM 152 171
FT TOPO_DOM 172 189
FT TRANSMEM 190 213
FT TOPO_DOM 214 227
FT TRANSMEM 228 249
FT TOPO_DOM 250 268
FT TRANSMEM 269 291
FT TOPO_DOM 292 314
FT TRANSMEM 315 334
FT TOPO_DOM 335 349
FT TRANSMEM 350 369
FT TOPO_DOM 370 415
FT CARBOHYD 38 38
FT CARBOHYD 45 45
FT CARBOHYD 78 78
FT CARBOHYD 90 90
FT CARBOHYD 98 98
FT DISULFID 30 54
FT DISULFID 44 87
FT DISULFID 68 102
FT SEQUENCE 415 AA; 47842 MW; 48D6704B31D4C013 CRC64;
Query Match 89.3%; Score 2136.5; DB 1; Length 415;
Best Local Similarity 90.8%; Pred. No. 4.6e-168;
Matches 403; Conservative 5; Mismatches 7; Indels 29; Gaps 1;
QY 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCESLSLASNTISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGRRRQLRLVKALLLGLNPVSTSLQDQCENLSLTSNVSLQCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCAPFYGVYRNTNNGYRCLANGSWAARVNTSECOILNEEKSKVHYHVAV 120
DB 61 GQLVVRPCAPFYGVYRNTNNGYRCLANGSWAARVNTSECOILNEEKSKVHYHVAV 120
QY 121 IINYLGHCHLSVALLVAVFLRLRPGCTHWGDAQDALEVGAPWSGAPQVRRSIRCLR 180
DB 121 IINYLGHCHLSVALLVAVFLRLRPGCTHWGDAQDALEVGAPWSGAPQVRRSIRCLR 151
QY 181 NIHNWNLISAFILRNATFWVQLTMSPEVHQSNVGCRLVTAAYNFPHVTFNFMFEGGC 240
DB 152 NIHNWNLISAFILRNATFWVQLTMSPEVHQSNVGCRLVTAAYNFPHVTFNFMFEGGC 211
QY 241 YLHTAIVLVTSTDRLRKWFICIGWGPPIIIVAWAIGKLYYDNEKWCWFGKRGVYTDYI 300
DB 212 YLHTAIVLVTSTDRLRKWFICIGWGPPIIIVAWAIGKLYYDNEKWCWFGKRGVYTDYI 271
QY 301 YQGPMILVLLINFIPLFNVIILMTKLRSTSETIQRKAVKATVLLPLLIGITYMLFF 360
DB 272 YQGPMILVLLINFIPLFNVIILMTKLRSTSETIQRKAVKATVLLPLLIGITYMLFF 331
QY 361 VNFGEDEVSRVVFYFNFSFLESFGQFVSVFYFCFLNSVEVSAIRKRWHRQDKHSIRARV 420
DB 332 VNFGEDEVSRVVFYFNFSFLESFGQFVSVFYFCFLNSVEVSAIRKRWHRQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444

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|||||
392 ARAMSIPTSPTRVSHSIKQSTAV 415

RESULT 9
Q9BGU4 BOVIN
ID Q9BGU4 BOVIN PRELIMINARY; PRT; 415 AA.
AC Q9BGU4;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DE Corticotropin-releasing hormone receptor.
GN Name=CRFR;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Holstein;
RA Takata M., Sekikawa K.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB055434; BAB21864.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR003052; CRF1 receptor.
DR InterPro; IPR003051; GPCR secretin.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR01279; CRFRECEPTOR.
DR PRINTS; PR01280; CRFRECEPTOR1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE. 415 AA; 47754 MW; 4A54A3DCE6CF2319 CRC64;

Query Match 89.3%; Score 2126.5; DB 2; Length 415;
Best Local Similarity 90.5%; Pred. No. 4.6e-168;
Matches 402; Conservative 7; Mismatches 6; Indels 29; Gaps 1;

QY 1 MCGHPQLRLVKALLLGLNPVSASLQDQHCESLSLASNTSGLOCNASVDLIGTCWPRSPA 60
DB 1 MGRRPQLRLVKALLLGLNLSISASLQDQHCESLSVASNSVGLQCNASVDLIGTCWQPSA 60

QY 61 GQLVVRPCPAFFGVRYNTNTNGYRECLANGSWAARVNYSECOEILNEEKSKSVHYHVAV 120
DB 61 GQLVVRPCLVFFGVRYNTNTNGYRECLANGTWAARVNYSECOEILNEEKSKSVHYHVAV 120

QY 121 IINYLGHCSLVALLVAFVLFLRLPGCTHWGDAQDALEVGAPWNSGAPPQVRRSTRCLR 180
DB 121 IINYLGHCSLSAALLVAFVLFLRL-----RSRCLR 151

QY 181 NIHNWNLISAFILRNATFVVQVTMSPEVHQSNGVGRCLVTAAYNFVHTNFFWMEGEC 240
DB 152 NIHNWNLISAFILRNATFVVQVTMSPEVHQSNGVGRCLVTAAYNFVHTNFFWMEGEC 211

QY 241 YLHTAIVLTSTDRLRKMFICIGWGPFPPIIVAWAIGKLYYDNEKCFKRGVYTDYI 300
DB 212 YLHTAIVLTSTDRLRKMFICIGWGPFPPIIVAWAIGKLYYDNEKCFKRGVYTDYI 271

QY 301 YQGPMILVLLINFIPLFNIVRIIMTKLRASTSETTQYRKAVKATVLLPLLGITMYLFF 360
DB 272 YQGPMILVLLINFIPLFNIVRIIMTKLRASTSETTQYRKAVKATVLLPLLGITMYLFF 331

QY 361 VNPGEDEVSRVVFIYFNSEFLSFQGFVSVFCFLNSEVRSAIRKRWHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVVFIYFNSEFLSFQGFVSVFCFLNSEVRSAIRKRWHRWQDKHSIRARV 391

QY 421 ARAMSIPTSPTRVSHSIKQSTAV 444
DB 392 ARAMSIPTSPTRVSHSIKQSTAV 415

RESULT 10
CRFR1 SHEEP
ID CRFR1 SHEEP STANDARD; PRT; 415 AA.
AC O62772;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)
DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).
GN Name=CRHR1;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=9907928; PubMed=9863624; DOI=10.1016/S0303-7207(98)00157-9;
RA Myers D.A., Trinh J.V., Myers T.R.;
RT "Structure and function of the ovine type 1 corticotropin releasing
factor receptor (CRF1) and a carboxyl-terminal variant.";
RL Mol. Cell. Endocrinol. 144:21-35(1998).
CC -!- FUNCTION: This is a receptor for corticotropin releasing factor.
Shows high-affinity CRF binding. The activity of this receptor is
mediated by G proteins which activate adenylyl cyclase.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: Carboxyl-terminal Ser or Thr residues may be phosphorylated.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.

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removed.

EMBL; AF054582; AAC08027.1; -; mRNA.
DR InterPro; IPR003052; CRF1_receptor.
DR InterPro; IPR003051; CRF_receptor.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR PANTHER; PTHR12011:SF16; CRF_receptor; 1.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR01279; CRFRECEPTOR.
DR PRINTS; PR01280; CRFRECEPTOR1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; FALSE_NEG.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW G-protein coupled receptor; Glycoprotein; Phosphorylation; Receptor;
Signal; Transducer; Transmembrane.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 415 Corticotropin releasing factor receptor
1.
FT TOPO_DOM 24 121 Extracellular (Potential).
FT TRANSMEM 122 142 1 (Potential).
FT TOPO_DOM 143 151 Cytoplasmic (Potential).
FT TRANSMEM 152 171 2 (Potential).
FT TOPO_DOM 172 189 Extracellular (Potential).
FT TRANSMEM 190 213 3 (Potential).
FT TOPO_DOM 214 227 Cytoplasmic (Potential).
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FT	TRANSMEM	228	249	4 (Potential).	
FT	TOPO_DOM	250	268	Extracellular (Potential).	
FT	TRANSMEM	269	291	5 (Potential).	
FT	TOPO_DOM	292	314	Cytoplasmic (Potential).	
FT	TRANSMEM	315	334	6 (Potential).	
FT	TOPO_DOM	335	349	Extracellular (Potential).	
FT	TRANSMEM	350	369	7 (Potential).	
FT	TOPO_DOM	370	415	Cytoplasmic (Potential).	
FT	CARBOHYD	38	38	N-linked (GLCNAC. . .) (Potential).	
FT	CARBOHYD	45	45	N-linked (GLCNAC. . .) (Potential).	
FT	CARBOHYD	51	51	N-linked (GLCNAC. . .) (Potential).	
FT	CARBOHYD	78	78	N-linked (GLCNAC. . .) (Potential).	
FT	CARBOHYD	90	90	N-linked (GLCNAC. . .) (Potential).	
FT	CARBOHYD	98	98	N-linked (GLCNAC. . .) (Potential).	
FT	DISULFID	30	54	By similarity.	
FT	DISULFID	44	87	By similarity.	
FT	DISULFID	68	102	By similarity.	
SQ	SEQUENCE	415 AA;	47559 MW;	FA5P652D12B4CDC4 CRC64;	
Query Match					
Best Local Similarity 87.8%; Score 2086.5; DB 1; Length 415;					
Matches 394; Conservative 11; Mismatches 10; Indels 29; Gaps 1;					
QY	1	MGCHPOLRLVKALLLGLNPVSASLODQHCESLSLASNISGLQCNASVDLIGTCWPRSPA	60		
DB	1	MGRRPQLRLVKALLLGLNLSISASLODQHCESLSLASNISGLQCNASVDLIGTCWQPSA	60		
QY	61	GLQVVRPCPAFFGVRYNTNTNGVRECLANGSWAARVNVSECOEILNEEKKSVHYHVAV	120		
DB	61	GLQVVRPCVFFGVRYNTNTNGVRECLANGVCLANGVWVNVSECOEILNEEKKSVHYHVAV	120		
QY	121	IINYLGHCSLVALVAVFLRLRPGCTHWGDAQDALEVGAPWPGAPQVRRSIRCLR	180		
DB	121	IINYLGHCSLVALVAVFLRLRPGCTHWGDAQDALEVGAPWPGAPQVRRSIRCLR	180		
QY	181	NIHWNLSAFLRNATFVQVQTMSPVHQSNGVWGLVTAAYNYPHVTNPFWMFEGGC	240		
DB	181	NIHWNLSAFLRNATFVQVQTMSPVHQSNGVWGLVTAAYNYPHVTNPFWMFEGGC	240		
QY	241	YLHTAVLVYSTDLRKWFCICIGWVPPPIIIVAWAIGKLYDNEKCFKRPQGVYTDYI	300		
DB	241	YLHTAVLVYSTDLRKWFCICIGWVPPPIIIVAWAIGKLYDNEKCFKRPQGVYTDYI	300		
QY	301	YQGPMLVLLINIFILNIVRIILMTKLRASTTSETIQYKAVKATLVLLPLLGITWMLFF	360		
DB	301	YQGPMLVLLINIFILNIVRIILMTKLRASTTSETIQYKAVKATLVLLPLLGITWMLFF	360		
QY	361	VNPGEDEVSRVFIYFNSFLESFQGPVSVFYCFNLSEVSRAIRKRWQDKHSIRARV	420		
DB	361	VNPGEDEVSRVFIYFNSFLESFQGPVSVFYCFNLSEVSRAIRKRWQDKHSIRARV	420		
QY	421	ARANSIPTSPTRVSFHSIKOSTAV 444			
DB	421	ARANSIPTSPTRVSFHSIKOSTAV 415			
RESULT 11					
CRF1 CHICK STANDARD; PRT; 420 AA.					
AC	Q90812;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	13-SEP-2005 (Rel. 48, Last annotation update)				
DE	Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)				
DE	(Corticotropin-releasing hormone receptor 1) (CRH-R 1).				
GN	Name=CRF1;				
OS	Gallus gallus (Chicken).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
OC	Gallus.				
OX	NCBI_TaxID=9031;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA].				

RX	MEDLINE=96107136; PubMed=8536612; DOI=10.1210/en.137.1.192;	
RA	Yu J., Xie L.Y., Abou-Samra A.-B.;	
RT	"Molecular cloning of a type A chicken corticotropin-releasing factor	
RT	receptor with high affinity for urotensin I.";	
RL	Endocrinology 137:192-197(1996).	
CC	-I- FUNCTION: This is a receptor for corticotropin releasing factor.	
CC	Shows high-affinity binding for urotensin I. The activity of this	
CC	receptor is mediated by G proteins which activate adenylyl	
CC	cyclase.	
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.	
CC	-I- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.	
CC	-----	
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use as long as its content is in no way modified and this statement is not	
CC	removed.	
CC	-----	
DR	EMBL; L41563; AAA96656.1; -; Genomic DNA.	
DR	Ensembl; ENSGALG00000000371; Gallus_gallus.	
DR	InterPro; IPR003052; CRF1_receptor.	
DR	InterPro; IPR003051; CRF_receptor.	
DR	InterPro; IPR000832; GPCR_secretin.	
DR	InterPro; IPR001879; hormn_receptor.	
DR	PANTHER; PTHR12011:SF16; CRF_receptor; 1.	
DR	Pfam; PF00002; 7tm_2; 1.	
DR	Pfam; PF02793; HRM; 1.	
DR	PRINTS; PR01279; CRFRECEPTOR.	
DR	PRINTS; PR01280; CRFRECEPTOR.	
DR	PRINTS; PR00249; GPCRSECRETIN.	
DR	SMART; SM00008; Hormr; 1.	
DR	PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.	
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.	
DR	PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.	
DR	PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.	
KW	G-protein coupled receptor; Glycoprotein; Receptor; Signal;	
KW	Transducer; Transmembrane.	
FT	SIGNAL	1 28
FT	CHAIN	29 420
FT	FT	Potential.
FT	FT	Corticotropin releasing factor receptor
FT	FT	1.
FT	TOPO_DOM	29 126
FT	TRANSMEM	127 147
FT	TOPO_DOM	148 156
FT	TRANSMEM	157 176
FT	TOPO_DOM	177 194
FT	TRANSMEM	195 218
FT	TOPO_DOM	219 232
FT	TRANSMEM	233 254
FT	TOPO_DOM	255 273
FT	TRANSMEM	274 296
FT	TOPO_DOM	297 319
FT	TRANSMEM	320 339
FT	TOPO_DOM	340 354
FT	TRANSMEM	355 374
FT	TOPO_DOM	375 420
FT	CARBOHYD	43 43
FT	CARBOHYD	50 50
FT	CARBOHYD	83 83
FT	CARBOHYD	95 95
FT	CARBOHYD	103 103
FT	DISULFID	35 59
FT	DISULFID	49 92
FT	DISULFID	73 107
SQ	SEQUENCE	420 AA; 48600 MW; 8C5C92925F62316 CRC64;
Query Match		
Best Local Similarity 82.1%; Pred. No. 5.5e-153;		
Matches 366; Conservative 25; Mismatches 23; Indels 32; Gaps 2;		
QY	2	GGHPQLRLVKALL-LLGLNPVSASLODQHCESLSLASNISGLQCNASVDLIGTCWPRS 58
DB	4	GPRPALLLLPLQLAFLWDSFVAASIQGYCESLLPTTNTHTGQCNSVDLIGTCWPRS 63

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QY 59 PAGQVVRPCPAFFYGVRYNTNNGYRECLANGSMAARVNYSCQILNEEKSKVHYHV 118
DB 64 AVQQLVAPCPBYFYGVRYNTNNGYRECLANGSMAARVNYSCQILNEEKSKLHYHI 123
QY 119 AVIINYLGHCISIVALLVAFVFLRLRPGCTHGWDAQDALEVGAPWGPQVRRSIRC 178
DB 124 AVIINYLGHCISVGLTLLVAFVFLRML-----RSIRC 154
QY 179 LRNIHWNLSAIFLNATWVTVOLTMSPRVHOSNVGWCRLVTAAYNYPHVTNFFWMEGE 238
DB 155 LRNIHWNLSAIFLNATWVTVOLTMSPRVHOSNVGWCRLVTAAYNYPHVTNFFWMEGE 214
QY 239 GCYLHTAIVLTSTDLRKLKWMFCIGWGPFPPIIWAAGLKYDNEKWFGRPGVYTD 298
DB 215 GCYLHTAIVLTSTDLRKLKWMFCIGWGPFPPIIWAAGLKYDNEKWFGRAGVYTD 274
QY 299 YIYQGMILVLLINFLFNIVRLMTKLRASSTSETIYQVKAVKATLVLLPLLGITYML 358
DB 275 YIYQGMILVLLINFLFNIVRLMTKLRASSTSETIYQVKAVKATLVLLPLLGITYML 334
QY 359 PFYNPGEDEVSRVVFYFNSFLESFQGFVSVFYCFINSEVRSAIRKRWHRWQDKHSIRA 418
DB 335 PFYNPGEDEVSRVVFYFNSFLESFQGFVSVFYCFINSEVRSAIRKRWHRWQDKHSIRA 394
QY 419 RVARAMSIPTRVSVFHSIKQSTAV 444
DB 395 RVARAMSIPTRVSVFHSIKQSSAV 420
RESULT 12
Q98UC2_9TELE
AC Q98UC2_9TELE PRELIMINARY; PRT; 445 AA.
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Corticotropin releasing factor receptor 1.
OS Aneurus nebulosus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Siluriformes;
OC Ictaluridae; Aneurus.
OX NCBI_TaxID=27778;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21066341; PubMed=11145609; DOI=10.1210/en.142.1.446;
RA Arai M., Asail I.Q., Abou-Samra A.B.;
RT "Characterization of three corticotropin-releasing factor receptors in
RT catfish: a novel third receptor is predominantly expressed in
RT pituitary and urophysis."
RL Endocrinology 142:446-454(2001).
DR ENBL, AF229359; AAK01068.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR003052; CRF_receptor.
DR InterPro; IPR003051; CRF_receptor.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF02793; HRM_1.
DR PRINTS; PR01279; CRFRECEPTOR.
DR PRINTS; PR01280; CRFRECEPTOR1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; UNKNOWN_1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
DR Receptor.
SQ SEQUENCE 445 AA; 51062 MW; F17DA70BE22BB755 CRC64;
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Query Match 76.3%; Score 1817.5; DB 2; Length 445;
Best Local Similarity 82.9%; Pred. No. 2,3e-142;
Matches 339; Conservative 22; Mismatches 19; Indels 29; Gaps 1;
QY 36 ASNIGSLQCNASVDLIGTCWPRSPAGQLVVRPCPAFFYGVRYNTNNGYRECLANGSMAA 95
DB 66 SSNATGLPCNIGSIDIGTCWPRSNAGEIVSRPCPETFLGVRVYNTNNGYRECLANGTMAK 125
QY 96 RVNYSECEILNEEKSKVHYHVAVIINYLGHCISIVALLVAFVFLRLRPGCTHGWDAQ 155
DB 126 KNGYSQCQILNEEKSKLHYHIAVINYLGHCISIGALLVAFVFLRML----- 174
QY 156 DGALEVGAPWGPQVRRSIRCLNIHWNLSAIFLNATWVTVOLTMSPRVHOSNVG 215
DB 175 -----RMIRCLNIIHWNLSAIFLNATWVTVOLTMSPRVHOSNVG 216
QY 216 WCLRVTAAYNYPHVTNFFWMEGCVLHTAIVLTSTDLRKLKWMFCIGWGPFPPIIWA 275
DB 217 WCLRVTAAYNYPHVTNFFWMEGCVLHTAIVLTSTDLRKLKWMFCIGWGPFPPIIWA 276
QY 276 AIGKLYDNEKWFGRPGVYTDIYQGMILVLLINFLFNIVRLMTKLRASSTSET 335
DB 277 AIGKLYDNEKWFGRAGVYTDIYQGMILVLLINFLFNIVRLMTKLRASSTSET 336
QY 336 IOYKAVKATLVLLPLLGITYMLFFVNPGEDEVSRVVFYFNSFLESFQGFVSVFYCF 395
DB 337 IOYKAVKATLVLLPLLGITYMLFFVNPGEDEVSRVVFYFNSFLESFQGFVSVFYCF 396
QY 396 NSEVRSAIRKRWHRWQDKHSIRARVARAMSIPTRVSVFHSIKQSTAV 444
DB 397 NSEVRSAIRKRWHRWQDKHSIRARVARAMSIPTRVSVFHSIKQSSAV 445
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AC Q8AWA2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Corticotropin-releasing factor receptor type 1.
GN Name=crfr1;
OS Oncorhynchus keta (Chum salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Pohl S., Darlison M.G., Lederis K., Richter D.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277157; CAC81753.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR003052; CRF_receptor.
DR InterPro; IPR003051; CRF_receptor.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR01279; CRFRECEPTOR.
DR PRINTS; PR01280; CRFRECEPTOR1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; UNKNOWN_1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
DR Receptor.
KW
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Db 276 VILVLLINFIENIVIRILMTKLRASSTSETIQYKAVKATVLLPLLGITVYMLFFVTPG 335
QY 365 EDESVRVVFIYFNSPLESFQGFVSVFYCPLNSEVRSATRKRWHRWQDKHSIRARVAM 424
Db 336 EDBISRIVFIYFNSPLESFQGFVSVFYCPLNSEVRSATRKRWHRWQDKHSIRARVAM 395
QY 425 SIPTSPTRVSHSIKOSTAV 444
Db 396 SIPTSPTRISFHSIKOSSAI 415

RESULT 15
Q68Y61_RANCA
ID Q68Y61_RANCA PRELIMINARY; PRT; 416 AA.
AC Q68Y61;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Corticotropin releasing factor receptor type 1.
GN Name=CRFR-1.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana;
OC Aquarana.
OX NCBI_TaxID=8400;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ito Y., Ogata D., Hasunuma I., Kikuyama S.;
RT "molecular cloning of two corticotropin releasing factor receptors
RT from bullfrog.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB188110; BAD36783.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR003052; CRF1_receptor.
DR InterPro; IPR003051; CRF_receptor.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HEM_1.
DR PRINTS; PR01279; CRFRECEPTOR.
DR PRINTS; PR01280; CRFRECEPTORL.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 416 AA; 47798 MW; C7F085BD71916E1B CRC64;

Query Match 75.1%; Score 1789; DB 2; Length 416;
Best Local Similarity 75.9%; Pred. No. 4.9e-140;
Matches 337; Conservative 37; Mismatches 32; Indels 38; Gaps 4;

QY 9 LVKALLLLGLNVPVSA-----SLQDQHCESLSLAGNISGLQNASVDLIGTCWPRSPAG 61
Db 3 LSKSPLLLFVQVITAGVSLATSIQDQ-CENLQSSNITGLACNISIDMIGTCWPRTPAG 61
QY 62 QLVVR-PCPAFFYGVNTNNGYRECLANGSWAARNYISECOELLNEEKSKVHYHVAV 120
Db 62 QLGGHGCPCEPFYFGVQVNTNGYRECLNGSWAGRGDYTCQCEILKQEKSKVHYHAI 121
QY 121 IINVLGHCSLVALLVAFVLFLRLPGCTHWGDAQDALEVGAPWSPQVRRSIRCLR 180
Db 122 VINFLGHSISLCAALLVAFTLFLRL-----RSIRCLR 152
QY 181 NIHWNLISAFILRNATFVVVLVTMTSPSEVHOSNVGWCRLVTAANYPHVTNFFWMEGEC 240
Db 153 NIIHWNLITAFILRNITFWVQLTSLQEAHDSNVVWCRLVTIAHNYFYVTNFFWMEGEC 212
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QY 241 YLHTAIVLTYSTDLRLKWMFICIGWGPPEPIIWAAGKLYYDNEKCMFGKPGVYVTDVI 300
Db 213 YLHTAIVLTYSTDLRLKWMFICIGWGPPEPIIWAAGKLYYDNEKCMFGKAGVYVTDI 272
QY 301 YQGPMLVLLINFIENIVIRILMTKLRASSTSETIQYKAVKATVLLPLLGITVYMLFF 360
Db 273 YQGPVILVLLINFIENIVIRILMTKLRASSTSETIQYKAVKATVLLPLLGITVYMLFF 332
QY 361 VNPGEDEVSRVFIYFNSPLESFQGFVSVFYCPLNSEVRSATRKRWHRWQDKHSIRARV 420
Db 333 VTPGEDEVSRIVFIYFNSPLESFQGFVSVFYCPLNSEVRSATRKRWHRWQDKHSIRARV 392
QY 421 ARAMSIPTSPTRVSHSIKOSTAV 444
Db 393 ARAMSIPTSPTRVSHSIKOSSAI 416

Search completed: March 16, 2006, 17:20:15
Job time : 234 secs
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OM protein - protein search, using sw model

Run on: March 16, 2006, 17:20:34 ; Search time 47 Seconds
(without alignments)
781.021 Million cell updates/sec

Title: US-10-649-193-15
Perfect score: 2381
Sequence: 1 MGGHPQLRVKALLLGLNP.....SIPTSPTRVSFHSIKQSTAV 444

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2381	100.0	444	2	US-08-482-746-15
2	2381	100.0	444	2	US-09-580-734-15
3	2381	100.0	444	2	US-08-374-009-15
4	2381	100.0	444	2	US-09-191-724-15
5	2381	100.0	444	2	US-09-631-603-11
6	2186.5	91.8	415	1	US-08-110-286A-2
7	2186.5	91.8	415	2	US-08-482-746-2
8	2186.5	91.8	415	2	US-09-580-734-2
9	2186.5	91.8	415	2	US-08-374-009-2
10	2186.5	91.8	415	2	US-09-191-724-2
11	2186.5	91.8	415	2	US-09-799-978-2
12	2186.5	91.8	415	2	US-09-799-978-4
13	2180.5	91.6	415	2	US-09-826-509-483
14	2137.5	89.8	415	2	US-08-482-746-13
15	2137.5	89.8	415	2	US-09-580-734-13
16	2137.5	89.8	415	2	US-08-374-009-13
17	2137.5	89.8	415	2	US-09-191-724-13
18	2137.5	89.8	415	2	US-09-799-978-22
19	2126.5	89.3	415	1	US-08-110-286A-6
20	2126.5	89.3	415	2	US-08-981-189B-10
21	2126.5	89.3	415	2	US-08-482-746-6
22	2126.5	89.3	415	2	US-09-580-734-6
23	2126.5	89.3	415	2	US-08-374-009-6
24	2126.5	89.3	415	2	US-09-191-724-6
25	2126.5	89.3	415	2	US-08-799-978-16
26	2126.5	89.3	415	2	US-09-799-978-40
27	2092.5	87.9	401	2	US-09-799-978-8

28	2086.5	87.6	415	2	US-09-799-978-28	Sequence 28, Appl
29	1945	81.7	420	2	US-09-799-978-42	Sequence 42, Appl
30	1925.5	80.9	375	2	US-09-799-978-6	Sequence 6, Appl
31	1817.5	76.3	445	2	US-09-799-978-34	Sequence 34, Appl
32	1796.5	75.5	415	2	US-09-799-978-30	Sequence 30, Appl
33	1741.5	73.1	428	2	US-09-799-978-36	Sequence 36, Appl
34	1574.5	66.1	438	2	US-09-799-978-12	Sequence 12, Appl
35	1562	65.6	431	2	US-08-981-189B-13	Sequence 13, Appl
36	1562	65.6	431	2	US-09-881-401-2	Sequence 2, Appl
37	1561	65.6	405	2	US-09-799-978-38	Sequence 38, Appl
38	1556	65.4	431	1	US-08-381-433A-2	Sequence 4, Appl
39	1550.5	65.1	411	1	US-08-381-433A-4	Sequence 12, Appl
40	1550.5	65.1	411	2	US-08-981-189B-12	Sequence 18, Appl
41	1550.5	65.1	411	2	US-09-799-978-18	Sequence 4, Appl
42	1550.5	65.1	411	2	US-09-881-401-4	Sequence 12, Appl
43	1549.5	65.1	411	2	US-09-631-603-12	Sequence 20, Appl
44	1549	65.1	431	2	US-09-799-978-20	Sequence 14, Appl
45	1547.5	65.0	397	2	US-09-799-978-14	

ALIGNMENTS

RESULT 1
US-08-482-746-15
; Sequence 15, Application US/08482746B
; Patent No. 6399315
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; FILE REFERENCE: P41-90002
; CURRENT APPLICATION NUMBER: US/08/482,746B
; CURRENT FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: US 08/374,009
; EARLIER FILING DATE: 1995-01-17
; EARLIER APPLICATION NUMBER: US 08/353,537
; EARLIER FILING DATE: 1994-12-09
; EARLIER APPLICATION NUMBER: PCT/US94/05908
; EARLIER FILING DATE: 1994-05-25
; EARLIER APPLICATION NUMBER: US 08/110,286
; EARLIER FILING DATE: 1993-08-23
; EARLIER APPLICATION NUMBER: US 08/079,320
; EARLIER FILING DATE: 1993-06-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-482-746-15

Query Match	100.0%;	Score 2381;	DB 2;	Length 444;
Best Local Similarity	100.0%;	Pred. No. 1.2e-232;		
Matches 444;	Conservative	0;	Mismatches	0; Gaps 0;
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Db	1	MGGHPQLRVKALLLGLNPVSASLQDQCESLSLASNISGLQCNASVDLIGTCWPRSPA	60	
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Db	61	GQLVWRPCPAFFGVRYNTTNGYRECLANGSWAARNYSECOILNEEKKSVHYHAV	120	
Qy	121	IINVLGHCSLVALLVAFVLFLRLPCTHWGDQADGALFVGAPWPGAPFQVRRSIRCLR	180	
Db	121	IINVLGHCSLVALLVAFVLFLRLPCTHWGDQADGALFVGAPWPGAPFQVRRSIRCLR	180	

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DB 241 YLHTAIVLTYSTDRLRKWMFICIGMGVPPPIIIVAMAIGKLYYDNEKCMFQKRGVYTDYI 300
QY 301 YQGPMLVLVLLINFIPLFNIVRIILMTKLRASTTSETIOYRKAVKATVLLPLLGITTYMLPF 360
DB 301 YQGPMLVLVLLINFIPLFNIVRIILMTKLRASTTSETIOYRKAVKATVLLPLLGITTYMLPF 360
QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRQDKHSIRARV 420
DB 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRQDKHSIRARV 420
QY 421 ARAMSIPTSPTRVSVFHSIKOSTAV 444
DB 421 ARAMSIPTSPTRVSVFHSIKOSTAV 444

RESULT 2

US-09-580-734-15
; Sequence 15, Application US/09580734
; Patent No. 6482608
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; FILE OF INVENTION: CRF Receptor(s)
; FILE REFERENCE: Salk1748
; CURRENT APPLICATION NUMBER: US/09/580,734
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/191,724
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/374,009
; PRIOR FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: US 08/353,537
; PRIOR FILING DATE: 1994-12-09
; PRIOR APPLICATION NUMBER: PCT/US94/05908
; PRIOR FILING DATE: 1993-05-25
; PRIOR APPLICATION NUMBER: US 08/110,286
; PRIOR FILING DATE: 1993-08-23
; PRIOR APPLICATION NUMBER: US 08/079,320
; PRIOR FILING DATE: 1993-06-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-580-734-15

Query Match 100.0%; Score 2381; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 GQLVVRPCPAFFVGVRYNTNNGYRECLANGSWAARVNYSECOILNEEKSKVHYHVAV 120
QY 121 IINYLGHCSLVALLVAFVLFLRLRPGCTHWGDQADGALEVGAPWPGAPQVRRSIRCLR 180
DB 121 IINYLGHCSLVALLVAFVLFLRLRPGCTHWGDQADGALEVGAPWPGAPQVRRSIRCLR 180

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DB 241 YLHTAIVLTYSTDRLRKWMFICIGMGVPPPIIIVAMAIGKLYYDNEKCMFQKRGVYTDYI 300
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DB 301 YQGPMLVLVLLINFIPLFNIVRIILMTKLRASTTSETIOYRKAVKATVLLPLLGITTYMLPF 360
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DB 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRQDKHSIRARV 420
QY 421 ARAMSIPTSPTRVSVFHSIKOSTAV 444
DB 421 ARAMSIPTSPTRVSVFHSIKOSTAV 444

RESULT 3

US-08-374-009-15
; Sequence 15, Application US/08374009A
; Patent No. 6495343
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; FILE OF INVENTION: CRF Receptor(s)
; FILE REFERENCE: P41 9886
; CURRENT APPLICATION NUMBER: US/08/374,009A
; CURRENT FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: US 08/353,537
; PRIOR FILING DATE: 1994-12-09
; PRIOR APPLICATION NUMBER: US 08/079,320
; PRIOR FILING DATE: 1993-06-18
; PRIOR APPLICATION NUMBER: US 08/110,286
; PRIOR FILING DATE: 1993-08-23
; PRIOR APPLICATION NUMBER: PCT/US94/05908
; PRIOR FILING DATE: 1994-05-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-374-009-15

Query Match 100.0%; Score 2381; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	301	YOGPMILVLLINFLNFIPLFNIIVRLIMTKLRASPTSTIOYRKAVKATLVLLPLLGITTYMLPF	360
Db	301	YOGPMILVLLINFLNFIPLFNIIVRLIMTKLRASPTSTIOYRKAVKATLVLLPLLGITTYMLPF	360
Qy	361	VNPGEDSVRVVFIYFNFSFLSFQGFVFPYCFNLSEVSASIRKRWHRWQDKHSIRARV	420
Db	361	VNPGEDSVRVVFIYFNFSFLSFQGFVFPYCFNLSEVSASIRKRWHRWQDKHSIRARV	420
Qy	421	ARAGSIPTSPTRVSFHSIKQSTAV	444
Db	421	ARAGSIPTSPTRVSFHSIKQSTAV	444

Query Match	100.0%;	Score 2381;	DB 2;	Length 444;
Best Local Similarity	100.0%;	Pred. No. 1.2e-232;		
Matches 444;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MGGHPQLRLVKALLLLGILNVPASLSLOQDHCHESLSLASNISGLQCNASVDLIGTCWPRSPA	60	
Db	1	MGGHPQLRLVKALLLLGILNVPASLSLOQDHCHESLSLASNISGLQCNASVDLIGTCWPRSPA	60	
Qy	61	GLVVRPCPAFFYGVRYNTTNGYRECLANGSMAARVNYSECQILNEEKSKVHYHVAV	120	
Db	61	GLVVRPCPAFFYGVRYNTTNGYRECLANGSMAARVNYSECQILNEEKSKVHYHVAV	120	
Qy	121	IINYLGHICISLVALLVAFVLFLRLRPGCTHWGDAQDGALEVGAPWSGAPFVRRSIRCLR	180	
Db	121	IINYLGHICISLVALLVAFVLFLRLRPGCTHWGDAQDGALEVGAPWSGAPFVRRSIRCLR	180	
Qy	181	NITHWNLISAFILRNATFVVQLTMSPEVHOSNVGWCRLVTAAYNYFHTVTFNFMFGEGC	240	
Db	181	NITHWNLISAFILRNATFVVQLTMSPEVHOSNVGWCRLVTAAYNYFHTVTFNFMFGEGC	240	
Qy	241	YLHTAIVLTYSTDRLRKMFTICIGWGPFPPIIVAWAIGKLYYDREKWCWGRKPGPYTDYI	300	

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RESULT 5
US-09-631-603-11
; Sequence 11, Application US/09631603
; Patent No. 6733990
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Lloyd, Clare
; APPLICANT: Weich, Nadine
; TITLE OF INVENTION: 15571, A No. 6733990el GPCR-like Molecule of the
; TITLE OF INVENTION: Secretin-Like Family and Uses Thereof
; FILE REFERENCES: 5800-48A
; CURRENT APPLICATION NUMBER: US/09/631,603
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/515,781
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/146,916
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-631-603-11

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Query Match	100.0.0%;	Score 2391;	DB 2;	Length 444;
Best Local Similarity	100.0.0%;	Pred. No. 1.2e-232;		
Matches 444;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MGGHPOLRLVKALLLGLNLPVSASLODQHCEISLASNISGLQCNASVDLIGTCWRPSPA	60	
Db	1	MGGHPOLRLVKALLLGLNLPVSASLODQHCEISLASNISGLQCNASVDLIGTCWRPSPA	60	
Qy	61	GQLVWRPCPAFFYGVRYRNTTNGYRECLANGSWAARVNYSECQEILNBEKKSKVHYHAV	120	
Db	61	GQLVWRPCPAFFYGVRYRNTTNGYRECLANGSWAARVNYSECQEILNBEKKSKVHYHAV	120	
Qy	121	IINYLGHCISLVALLVAVFLFLRLPCTHWGDAQDGALEVGAPWSCAPFQVRRSIRCLR	180	
Db	121	IINYLGHCISLVALLVAVFLFLRLPCTHWGDAQDGALEVGAPWSCAPFQVRRSIRCLR	180	
Qy	181	NIHWNLISAFILRNATFVQVLTMGSEVHQSNVGCRLVTAAYNYPHVTNFFWFMGEGC	240	
Db	181	NIHWNLISAFILRNATFVQVLTMGSEVHQSNVGCRLVTAAYNYPHVTNFFWFMGEGC	240	
Qy	241	YLHTAIVLTVSTDRLRKWMCIFICIGWVPPFIIIVAWAIGKLYDNEKCFWGRKPGVYTDYI	300	
Db	241	YLHTAIVLTVSTDRLRKWMCIFICIGWVPPFIIIVAWAIGKLYDNEKCFWGRKPGVYTDYI	300	
Qy	301	YQGFPMILVLLINFIPLFNIVRILMTKLRASTSETIOYRKAVKATLVLLPLLGITYMLFF	360	
Db	301	YQGFPMILVLLINFIPLFNIVRILMTKLRASTSETIOYRKAVKATLVLLPLLGITYMLFF	360	
Qy	361	VNPGDEVSRVFIYFNPSFLESFGGFVPSVFCPLNSEVRSATKRWHRWQDDKHSIRARV	420	
Db	361	VNPGDEVSRVFIYFNPSFLESFGGFVPSVFCPLNSEVRSATKRWHRWQDDKHSIRARV	420	
Qy	421	ARAMSIPTSPTRVSHSIKOSTAV	444	

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Db      421 ARAMSIPTSPTRVSHSIKQSTAV 444
|||||
RESULT 6
US-08-110-286A-2
; Sequence 2, Application US/08110286A
; Patent No. 5728545
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
; TITLE OF INVENTION: CRF RECEPTOR(S)
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,286A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/079,320
; FILING DATE: 18-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9439
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-110-286A-2

Query Match          91.8%; Score 2186.5; DB 1; Length 415;
Best Local Similarity 93.5%; Pred. No. 5.7e-213;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY      1 MGGHPQLRLVKALLGLNPVSASLQDQHCEISLSASNISGLQCNASVDLIGTCWPRSPA 60
Db      1 MGGHPQLRLVKALLGLNPVSASLQDQHCEISLSASNISGLQCNASVDLIGTCWPRSPA 60
QY      61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIINEEKSKVHYHVAV 120
Db      61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIINEEKSKVHYHVAV 120
QY      121 IINYLGHCI SLVALLVAVFLRLRPGCTHWGDAQDGALEVGAPWGSAPFQVRRSRICLR 180
Db      121 IINYLGHCI SLVALLVAVFLRLRPGCTHWGDAQDGALEVGAPWGSAPFQVRRSRICLR 180
QY      181 NIHNWNLISAFILRNATWFFVOLTMSPVHQSNVGCRLVTAAYNFYHVTNPFWMFGECC 240
Db      152 NIHNWNLISAFILRNATWFFVOLTMSPVHQSNVGCRLVTAAYNFYHVTNPFWMFGECC 211
QY      241 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKWCWFGKRGPGVYTDYI 300
Db      212 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKWCWFGKRGPGVYTDYI 271

Db      212 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKWCWFGKRGPGVYTDYI 271
QY      301 YQGPMLVLLINFIPLFNIVRILMTKLRASSTSETIOYRKAVKATVLLPLLGITVMLPF 360
Db      272 YQGPMLVLLINFIPLFNIVRILMTKLRASSTSETIOYRKAVKATVLLPLLGITVMLPF 331
QY      361 VNPGEDEVSRVVIYFENSFLESFQGFVSVFYCFNLNSEVRSAIRKWHRWQDKHSIRARV 420
Db      332 VNPGEDEVSRVVIYFENSFLESFQGFVSVFYCFNLNSEVRSAIRKWHRWQDKHSIRARV 391
QY      421 ARAMSIPTSPTRVSHSIKQSTAV 444
Db      392 ARAMSIPTSPTRVSHSIKQSTAV 415

RESULT 7
US-08-482-746-2
; Sequence 2, Application US/08482746B
; Patent No. 6399315
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: CRF Receptor(s)
; FILE REFERENCE: P41-90002
; CURRENT APPLICATION NUMBER: US/08/482,746B
; CURRENT FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: US 08/374,009
; EARLIER FILING DATE: 1995-01-17
; EARLIER APPLICATION NUMBER: US 08/353,537
; EARLIER FILING DATE: 1994-12-09
; EARLIER APPLICATION NUMBER: PCT/US94/05908
; EARLIER FILING DATE: 1994-05-25
; EARLIER APPLICATION NUMBER: US 08/110,286
; EARLIER FILING DATE: 1993-08-23
; EARLIER APPLICATION NUMBER: US 08/079,320
; EARLIER FILING DATE: 1993-06-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-482-746-2

Query Match          91.8%; Score 2186.5; DB 2; Length 415;
Best Local Similarity 93.5%; Pred. No. 5.7e-213;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY      1 MGGHPQLRLVKALLGLNPVSASLQDQHCEISLSASNISGLQCNASVDLIGTCWPRSPA 60
Db      1 MGGHPQLRLVKALLGLNPVSASLQDQHCEISLSASNISGLQCNASVDLIGTCWPRSPA 60
QY      61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIINEEKSKVHYHVAV 120
Db      61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIINEEKSKVHYHVAV 120
QY      121 IINYLGHCI SLVALLVAVFLRLRPGCTHWGDAQDGALEVGAPWGSAPFQVRRSRICLR 180
Db      121 IINYLGHCI SLVALLVAVFLRLRPGCTHWGDAQDGALEVGAPWGSAPFQVRRSRICLR 180
QY      181 NIHNWNLISAFILRNATWFFVOLTMSPVHQSNVGCRLVTAAYNFYHVTNPFWMFGECC 240
Db      152 NIHNWNLISAFILRNATWFFVOLTMSPVHQSNVGCRLVTAAYNFYHVTNPFWMFGECC 211
QY      241 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKWCWFGKRGPGVYTDYI 300
Db      212 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKWCWFGKRGPGVYTDYI 271
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QY 301 YQGPMLVLLINFIPLFNIVRIIMTKLRASSTTSETIOYRKAVKATVLLPLLGITVMLFF 360
DB 272 YQGPMLVLLINFIPLFNIVRIIMTKLRASSTTSETIOYRKAVKATVLLPLLGITVMLFF 331
QY 361 VNPGEDEVSRVVIYFNPSFLESFQGFVSVFYCFNLNSEVRSAIRKRWHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVVIYFNPSFLESFQGFVSVFYCFNLNSEVRSAIRKRWHRWQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444
DB 392 ARAMSIPTSPTRVSVFHSIKQSTAV 415

RESULT 8

US-09-580-734-2
; Sequence 2, Application US/09580734
; Patent No. 6482608
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: CRF Receptor(s)
; FILE REFERENCE: Salk1748
; CURRENT APPLICATION NUMBER: US/09/580,734
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/191,724
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/374,009
; PRIOR FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: US 08/353,537
; PRIOR FILING DATE: 1994-12-09
; PRIOR APPLICATION NUMBER: PCT/US94/05908
; PRIOR FILING DATE: 1993-05-25
; PRIOR APPLICATION NUMBER: US 08/110,286
; PRIOR FILING DATE: 1993-08-23
; PRIOR APPLICATION NUMBER: US 08/079,320
; PRIOR FILING DATE: 1993-06-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-580-734-2

Query Match 91.8%; Score 2186.5; DB 2; Length 415;
Best Local Similarity 93.5%; Pred. No. 5.7e-213;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;
QY 1 MGHQPQLRVKALLLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGHQPQLRVKALLLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GOLVVRPCPAFFYGVRYNTTNGVRECLANGSWAARVNYSECOBILNEEKSKVHYHAV 120
DB 61 GOLVVRPCPAFFYGVRYNTTNGVRECLANGSWAARVNYSECOBILNEEKSKVHYHAV 120
QY 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPFQVRRSIRCLR 180
DB 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPFQVRRSIRCLR 151
QY 181 NIHNWNLISAFILRNATVFWVQLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWFMGECC 240
DB 152 NIHNWNLISAFILRNATVFWVQLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWFMGECC 211
QY 241 YLHTAIVLTSTDRLRKWMFICIGWGPFPPIIVAWAIGKLYYDNEKWCWFGKRPVGYTDYI 300
DB 212 YLHTAIVLTSTDRLRKWMFICIGWGPFPPIIVAWAIGKLYYDNEKWCWFGKRPVGYTDYI 271

QY 301 YQGPMLVLLINFIPLFNIVRIIMTKLRASSTTSETIOYRKAVKATVLLPLLGITVMLFF 360
DB 272 YQGPMLVLLINFIPLFNIVRIIMTKLRASSTTSETIOYRKAVKATVLLPLLGITVMLFF 331
QY 361 VNPGEDEVSRVVIYFNPSFLESFQGFVSVFYCFNLNSEVRSAIRKRWHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVVIYFNPSFLESFQGFVSVFYCFNLNSEVRSAIRKRWHRWQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444
DB 392 ARAMSIPTSPTRVSVFHSIKQSTAV 415

RESULT 9

US-08-374-009-2
; Sequence 2, Application US/08374009A
; Patent No. 6495343
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: CRF Receptor(s)
; FILE REFERENCE: P41 9886
; CURRENT APPLICATION NUMBER: US/08/374,009A
; PRIOR FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: US 08/353,537
; PRIOR FILING DATE: 1994-12-09
; PRIOR APPLICATION NUMBER: US 08/079,320
; PRIOR FILING DATE: 1993-06-18
; PRIOR APPLICATION NUMBER: US 08/110,286
; PRIOR FILING DATE: 1993-08-23
; PRIOR APPLICATION NUMBER: PCT/US94/05908
; PRIOR FILING DATE: 1994-05-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-374-009-2

Query Match 91.8%; Score 2186.5; DB 2; Length 415;
Best Local Similarity 93.5%; Pred. No. 5.7e-213;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY 1 MGHQPQLRVKALLLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGHQPQLRVKALLLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GOLVVRPCPAFFYGVRYNTTNGVRECLANGSWAARVNYSECOBILNEEKSKVHYHAV 120
DB 61 GOLVVRPCPAFFYGVRYNTTNGVRECLANGSWAARVNYSECOBILNEEKSKVHYHAV 120
QY 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPFQVRRSIRCLR 180
DB 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPFQVRRSIRCLR 151
QY 181 NIHNWNLISAFILRNATVFWVQLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWFMGECC 240
DB 152 NIHNWNLISAFILRNATVFWVQLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWFMGECC 211
QY 241 YLHTAIVLTSTDRLRKWMFICIGWGPFPPIIVAWAIGKLYYDNEKWCWFGKRPVGYTDYI 300
DB 212 YLHTAIVLTSTDRLRKWMFICIGWGPFPPIIVAWAIGKLYYDNEKWCWFGKRPVGYTDYI 271
QY 301 YQGPMLVLLINFIPLFNIVRIIMTKLRASSTTSETIOYRKAVKATVLLPLLGITVMLFF 360
DB 272 YQGPMLVLLINFIPLFNIVRIIMTKLRASSTTSETIOYRKAVKATVLLPLLGITVMLFF 331

[illegible]

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RESULT 10
US-09-191-724-2
; Sequence 2, Application US/09191724
; Patent No. 6638905
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping A.
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: CRP Receptor(s)
; FILE REFERENCE: Salk1748
; CURRENT APPLICATION NUMBER: US/09/191,724
; CURRENT FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: US 08/374,009
; EARLIER FILING DATE: 1995-01-17
; EARLIER APPLICATION NUMBER: US 08/353,537
; EARLIER FILING DATE: 1994-12-09
; EARLIER APPLICATION NUMBER: PCT/US94/05908
; EARLIER FILING DATE: 1993-05-25
; EARLIER APPLICATION NUMBER: US 08/110,286
; EARLIER FILING DATE: 1993-08-23
; EARLIER APPLICATION NUMBER: US 08/079,320
; EARLIER FILING DATE: 1993-06-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-191-724-2

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Query Match	91.8%; Score 2186.5; DB 2; Length 415;
Best Local Similarity	93.5%; Pred. No. 5.7e-213;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;	
Qy 1	MGGHPQLRLVKALLLGLNPVSASLODQHCEISLASNISGLQCNASVDLIGTCWPRSPA 60
Db 1	MGGHPQLRLVKALLLGLNPVSASLODQHCEISLASNISGLQCNASVDLIGTCWPRSPA 60
Qy 61	GQLVVRPCPAFFYQVRVNTTNGVRECLANGSNAARVNYSECILNEEKSKVHYHVAV 120
Db 61	GQLVVRPCPAFFYQVRVNTTNGVRECLANGSNAARVNYSECILNEEKSKVHYHVAV 120
Qy 121	IINYLGHCISILVALLVAVFLRLRPGCTHWGDQADGALEVGAPWSGAPQVRRSIRCLR 180
Db 121	IINYLGHCISILVALLVAVFLRL-----RSIRCLR 151
Qy 181	NIHWNLIISAFILRNATWFFVQLTMSPEVHQSNVGMCRVLTAAVNYFHVTFNFMFGECC 240
Db 152	NIHWNLIISAFILRNATWFFVQLTMSPEVHQSNVGMCRVLTAAVNYFHVTFNFMFGECC 211
Qy 241	YLHTAIVLVTSTDBLRKMMFCICGWGVPPIIIVAWAIGKLYYDNEKCFWGRKGVYTDYI 300
Db 212	YLHTAIVLVTSTDBLRKMMFCICGWGVPPIIIVAWAIGKLYYDNEKCFWGRKGVYTDYI 271
Qy 301	YQGMILVLLINFIIFLENIVRILMTKLRASTSETIOYRKAVKATLVLLPLLGITYMLFF 360
Db 272	YQGMILVLLINFIIFLENIVRILMTKLRASTSETIOYRKAVKATLVLLPLLGITYMLFF 331
Qy 361	VNFGEDSVSRVVFYIFNFSPLSFQGFVFSYPCFINSSEVSASIRKRWHRWQDKHSIRARV 420

[illegible]

Query Match	91.8%	Score 2186.5	DB 2	Length 415
Best Local Similarity	93.5%	Pred. No. 5.7e-213		
Matches 415	Conservative 0	Mismatches 0	Indels 29	Gaps 1
Qy	1	MGGHPQLRVKALLIGLNPVSASLDQHCESLSTASNTSGLCNASVDLIGTCWPRSPA	60	
Db	1	MGGHPQLRVKALLIGLNPVSASLDQHCESLSTASNTSGLCNASVDLIGTCWPRSPA	60	
Qy	61	GQLVVRPCPAFFVGVRYNTTNGRYRCLANGSWAARVNTSECOEILNEEKSKSVKVVHAV	120	
Db	61	GQLVVRPCPAFFVGVRYNTTNGRYRCLANGSWAARVNTSECOEILNEEKSKSVKVVHAV	120	
Qy	121	IINYLGHICISLVALLVAFVLFRLRPGCTHMGDQDGALEVGAPWSGAPQVRRSIRCLR	180	
Db	121	IINYLGHICISLVALLVAFVLFRL-----RSIRCLR	151	
Qy	181	NIHWNLIISAFILRNATWFWQLTNSPEVHQSNVGHCRLVTAAYNTFHVNTNPFWMFEGGC	240	
Db	152	NIHWNLIISAFILRNATWFWQLTNSPEVHQSNVGHCRLVTAAYNTFHVNTNPFWMFEGGC	211	
Qy	241	YLHTALVLTYSTDLRKRKMPICIGMGVPPPIIVAWAIGKLYDNEKCFWGRPGVVTDYI	300	
Db	212	YLHTALVLTYSTDLRKRKMPICIGMGVPPPIIVAWAIGKLYDNEKCFWGRPGVVTDYI	271	
Qy	301	YQGPMLVLLINFIPLFNIVRLMTKLRASSTSETIQYRKAVKATLVLLPLLGITVYMLFF	360	
Db	272	YQGPMLVLLINFIPLFNIVRLMTKLRASSTSETIQYRKAVKATLVLLPLLGITVYMLFF	331	
Qy	361	VNPGEDSVSRVFIYFNSEFLSEFQGFVSVFYCFNLSEVRSAIRKRWHRMQDKHSIRARV	420	
Db	332	VNPGEDSVSRVFIYFNSEFLSEFQGFVSVFYCFNLSEVRSAIRKRWHRMQDKHSIRARV	391	
Qy	421	ARAMSIPTGPTRVSPHSIIKQSTAV	444	
Db	392	ARAMSIPTGPTRVSPHSIIKQSTAV	415	

RESULT 12
US-09-799-978-4
; Sequence 4, Application US/09799978
; Patent No. 6670140
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell

US-09-826-509-483

Query Match 91.8%; Score 2186.5; DB 2; Length 415;
Best Local Similarity 93.5%; Pred. No. 5.7e-213;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GOLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKSKVHYHVA 120
DB 61 GOLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKSKVHYHVA 120
QY 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDALEVGAPWPGAPFQVRRSIRCLR 180
DB 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDALEVGAPWPGAPFQVRRSIRCLR 180
QY 181 NIHNWLIISAFILRNATFWVOLTMSPVHQSNGVWCRVLTAAAYNFHVTFNPFWMFGECC 240
DB 152 NIHNWLIISAFILRNATFWVOLTMSPVHQSNGVWCRVLTAAAYNFHVTFNPFWMFGECC 211
QY 241 YLHTAIVLTYSTDLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCFKRGFVYTDYI 300
DB 212 YLHTAIVLTYSTDLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCFKRGFVYTDYI 271
QY 301 YQGPMLVLLINFIPLFNIRILMTKLRATSTSETTOYRKAVKATVLLPLLIGITMFLFF 360
DB 272 YQGPMLVLLINFIPLFNIRILMTKLRATSTSETTOYRKAVKATVLLPLLIGITMFLFF 331
QY 361 VNPGEDEVSRVVIYNSFLESFQGFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVVIYNSFLESFQGFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSHSIKQSTAV 444
DB 392 ARAMSIPTSPTRVSHSIKQSTAV 415

RESULT 13

US-09-826-509-483
; Sequence 483, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 483
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-826-509-483

Query Match 91.6%; Score 2180.5; DB 2; Length 415;
Best Local Similarity 93.2%; Pred. No. 2.3e-212;
Matches 414; Conservative 0; Mismatches 1; Indels 29; Gaps 1;

QY 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
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QY 61 GOLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKSKVHYHVA 120
DB 61 GOLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKSKVHYHVA 120
QY 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDALEVGAPWPGAPFQVRRSIRCLR 180
DB 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDALEVGAPWPGAPFQVRRSIRCLR 180
QY 181 NIHNWLIISAFILRNATFWVOLTMSPVHQSNGVWCRVLTAAAYNFHVTFNPFWMFGECC 240
DB 152 NIHNWLIISAFILRNATFWVOLTMSPVHQSNGVWCRVLTAAAYNFHVTFNPFWMFGECC 211
QY 241 YLHTAIVLTYSTDLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCFKRGFVYTDYI 300
DB 212 YLHTAIVLTYSTDLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCFKRGFVYTDYI 271
QY 301 YQGPMLVLLINFIPLFNIRILMTKLRATSTSETTOYRKAVKATVLLPLLIGITMFLFF 360
DB 272 YQGPMLVLLINFIPLFNIRILMTKLRATSTSETTOYRKAVKATVLLPLLIGITMFLFF 331
QY 361 VNPGEDEVSRVVIYNSFLESFQGFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVVIYNSFLESFQGFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSHSIKQSTAV 444
DB 392 ARAMSIPTSPTRVSHSIKQSTAV 415

RESULT 14

US-08-482-746-13
; Sequence 13, Application US/08482746B
; Patent No. 6399315
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: CRF Receptor(s)
; FILE REFERENCE: P41-90002
; CURRENT APPLICATION NUMBER: US/08/482,746B
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: US 08/374,009
; EARLIER FILING DATE: 1995-01-17
; EARLIER APPLICATION NUMBER: US 08/353,537
; EARLIER FILING DATE: 1994-12-09
; EARLIER APPLICATION NUMBER: PCT/US94/05908
; EARLIER FILING DATE: 1994-05-25
; EARLIER APPLICATION NUMBER: US 08/110,286
; EARLIER FILING DATE: 1993-08-23
; EARLIER APPLICATION NUMBER: US 08/079,320
; EARLIER FILING DATE: 1993-06-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-482-746-13

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 16, 2006, 17:21:14 ; Search time 168 Seconds
(without alignments)
1104.263 Million cell updates/sec

Title: US-10-649-193-15
Perfect score: 2381
Sequence: 1 MGGHPQLRLVKALLLGLNP.....SIPTSPTRVFSHSIKQSTAV 444

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_Main:*

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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2381	100.0	444	3	US-09-853-386-132
2	2381	100.0	444	3	US-09-853-386-136
3	2381	100.0	444	3	US-09-191-724-15
4	2381	100.0	444	4	US-10-242-822B-2
5	2381	100.0	444	4	US-10-649-193-15
6	2324	97.6	447	4	US-10-232-798-708
7	2186.5	91.8	415	3	US-09-191-724-2
8	2186.5	91.8	415	3	US-09-799-978-2
9	2186.5	91.8	415	3	US-09-799-978-4
10	2186.5	91.8	415	4	US-10-242-822B-1
11	2186.5	91.8	415	4	US-10-649-193-2
12	2186.5	91.8	415	4	US-10-649-852-2
13	2186.5	91.8	415	4	US-10-649-852-4
14	2186.5	91.8	415	4	US-10-450-977-14
15	2180.5	91.6	415	3	US-09-826-509-483
16	2180.5	91.6	415	5	US-10-925-095-483
17	2137.5	89.8	415	3	US-09-853-386-131
18	2137.5	89.8	415	3	US-09-853-386-137
19	2137.5	89.8	415	3	US-09-853-386-138
20	2137.5	89.8	415	3	US-09-191-724-13
21	2137.5	89.8	415	3	US-09-799-978-22
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23	2137.5	89.8	415	4	US-10-649-193-13
24	2137.5	89.8	415	4	US-10-649-852-22
25	2126.5	89.3	415	3	US-09-853-386-130
26	2126.5	89.3	415	3	US-09-853-386-133
27	2126.5	89.3	415	3	US-09-853-386-134

28	2126.5	89.3	415	3	US-09-191-724-6
29	2126.5	89.3	415	3	US-09-818-009-10
30	2126.5	89.3	415	3	US-09-799-978-16
31	2126.5	89.3	415	3	US-09-799-978-40
32	2126.5	89.3	415	4	US-10-649-193-6
33	2126.5	89.3	415	4	US-10-649-852-16
34	2126.5	89.3	415	4	US-10-649-852-40
35	2092.5	87.9	401	3	US-09-853-386-127
36	2092.5	87.9	401	3	US-09-853-386-139
37	2092.5	87.9	401	3	US-09-799-978-8
38	2092.5	87.9	401	4	US-10-242-822B-4
39	2092.5	87.9	401	4	US-10-649-852-8
40	2086.5	87.6	415	3	US-09-853-386-128
41	2086.5	87.6	415	3	US-09-799-978-28
42	2086.5	87.6	415	4	US-10-649-852-28
43	1945	81.7	420	3	US-09-853-386-129
44	1945	81.7	420	3	US-09-799-978-42
45	1945	81.7	420	4	US-10-649-852-42

ALIGNMENTS

RESULT 1

US-09-853-386-132
; Sequence 132, Application US/09853386
; Patent No. US20020049151A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Evelyn
; APPLICANT: Breenihan, Barry
; APPLICANT: Conneely, Orla
; APPLICANT: Fitzgerald, Oliver
; TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR
; FILE REFERENCES: P01972US1
; CURRENT APPLICATION NUMBER: US/09/853,386
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/203645
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 132
; LENGTH: 444
; TYPE: PRT
; ORGANISM: HUMAN
; US-09-853-386-132

Query Match	100.0%;	Score 2381;	DB 3;	Length 444;
Best Local Similarity	100.0%;	Pred. No. 1.7e-217;	Mismatches 0;	Indels 0;
Matches 444;	Conservative 0;			Gaps 0;
QY	1	MGGHPQLRLVKALLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA	60	
Db	1	MGGHPQLRLVKALLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA	60	
QY	61	GLQVVRPCPAFFYGVRYNTNNNGYRECLANGSWAARVNYSECQILNEEKSKVHYHVAV	120	
Db	61	GLQVVRPCPAFFYGVRYNTNNNGYRECLANGSWAARVNYSECQILNEEKSKVHYHVAV	120	
QY	121	IINYLGHCTISLVALLVAFVFLRLRPGCTHWGDOADGALVGPWSGAPFQVRSIRCLR	180	
Db	121	IINYLGHCTISLVALLVAFVFLRLRPGCTHWGDOADGALVGPWSGAPFQVRSIRCLR	180	
QY	181	NIHWNILISAFILRNATFWVQLTMSPEVHQSNVGCRLVTAAYNYFHTNFFWMFGECC	240	
Db	181	NIHWNILISAFILRNATFWVQLTMSPEVHQSNVGCRLVTAAYNYFHTNFFWMFGECC	240	
QY	241	YLHTAIVLTSTDRLRKRMFCICGWGVPFPIIWAIAIGKLYYDNEKCFWPKRGVYTDYI	300	
Db	241	YLHTAIVLTSTDRLRKRMFCICGWGVPFPIIWAIAIGKLYYDNEKCFWPKRGVYTDYI	300	
QY	301	YQCPMLIVLLINFTIFLNIIVRLMTKLRASTTETIQYKAVKATILVLLPLLGITMYLFF	360	

Db 301 YQGPMLVLLNFIPLFNIVRLMTKLRSTTQYRKAVKATVLLPLLGITTYMLPF 360
QY 361 VNPGEDEVSRVVIYFNPSFLESQGFVSVFYCFNLSEVSARIRKRWHRWQDKHSIRARV 420
Db 361 VNPGEDEVSRVVIYFNPSFLESQGFVSVFYCFNLSEVSARIRKRWHRWQDKHSIRARV 420
QY 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444
Db 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444

RESULT 2
US-09-853-386-136
; Sequence 136, Application US/09853386
; Patent No. US20020049151A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Evelyn
; APPLICANT: Bresnahan, Barry
; APPLICANT: Conneely, Orla
; APPLICANT: Fitzgerald, Oliver
; TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR
; FILE OF INVENTION: Subfamily of Nuclear Transcription Factors
; FILE REFERENCE: P01972U81
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US/09/853,386
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 136
; LENGTH: 444
; TYPE: PRT
; ORGANISM: HUMAN
US-09-853-386-136

Query Match 100.0%; Score 2381; DB 3; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.7e-217;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGGHPQLRLVKALLLGLNPNVSLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
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Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSNAARVNYSECOEILNEEKSKVHYHVAV 120
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Db 121 IINYLGHICISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWGSAPFQVRRSIRCLR 180
QY 181 NIHNWNLISAFILRNATWVQVLTMSPEVHQSNVGCRLVTAAYNYFHVTFNPFMFGEBC 240
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QY 301 YQGPMLVLLNFIPLFNIVRLMTKLRSTTQYRKAVKATVLLPLLGITTYMLPF 360
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QY 361 VNPGEDEVSRVVIYFNPSFLESQGFVSVFYCFNLSEVSARIRKRWHRWQDKHSIRARV 420
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QY 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444
Db 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444

RESULT 3

US-09-191-724-15
; Sequence 15, Application US/09191724
; Patent No. US20020055617A1
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: CRF Receptor(s)
; FILE REFERENCE: Salk1748
; CURRENT APPLICATION NUMBER: US/09/191,724
; CURRENT FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: US 08/374,009
; EARLIER FILING DATE: 1995-01-17
; EARLIER APPLICATION NUMBER: US 08/353,537
; EARLIER FILING DATE: 1994-12-09
; EARLIER APPLICATION NUMBER: PCT/US94/05908
; EARLIER FILING DATE: 1993-05-25
; EARLIER APPLICATION NUMBER: US 08/110,286
; EARLIER FILING DATE: 1993-08-23
; EARLIER APPLICATION NUMBER: US 08/079,320
; EARLIER FILING DATE: 1993-06-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-191-724-15

Query Match 100.0%; Score 2381; DB 3; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.7e-217;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGHPQLRLVKALLLGLNPNVSLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
Db 1 MGGHPQLRLVKALLLGLNPNVSLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSNAARVNYSECOEILNEEKSKVHYHVAV 120
Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSNAARVNYSECOEILNEEKSKVHYHVAV 120
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Db 121 IINYLGHICISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWGSAPFQVRRSIRCLR 180
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Db 181 NIHNWNLISAFILRNATWVQVLTMSPEVHQSNVGCRLVTAAYNYFHVTFNPFMFGEBC 240
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QY 361 VNPGEDEVSRVVIYFNPSFLESQGFVSVFYCFNLSEVSARIRKRWHRWQDKHSIRARV 420
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QY 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444
Db 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444

RESULT 4
US-10-242-822B-2
; Sequence 2, Application US/10242822B

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; Publication No. US20030113799A1
; GENERAL INFORMATION:
; APPLICANT: Pisarchik, Alexander
; APPLICANT: Slocinski, Andrzej
; TITLE OF INVENTION: Variants of Corticotropin Releasing Hormone
; TITLE OF INVENTION: Receptor Type 1 and Uses Thereof
; FILE REFERENCE: D6420
; CURRENT APPLICATION NUMBER: US/10/242,822B
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/322,195
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 2
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: amino acid sequence of human CRH-R1 beta
; OTHER INFORMATION: gene: GenBank Accession No. US20030113799A1 L23333
US-10-242-822B-2

Query Match      100.0%; Score 2381; DB 4; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.7e-217;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGHQPQLRLVKALLLGLNPVSASLQDHCHESLSLASNISGLQCNASVDLIGTCWPRSPA 60

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DB 61 GQLVVRPCAPFFGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHYHVAV 120

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DB 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPQVRRSIRCLR 180

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DB 241 YLHTAIVLTSTDRLRKWMFICIGWGPFPPIIIVAWAIGKLYDNEKCFGRPGVYTDYI 300

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DB 301 YQGPMLVLVLLINFLFNIVIRILMTKLRASTTSETIQYKAVKATLVLLPLLGITYMLFF 360

QY 361 VNPGEDEVSRVVIYFNPSFLESFGQFPFVSFYCYFLNSEVRSAIRKRWHRWDKHSIRARV 420
DB 361 VNPGEDEVSRVVIYFNPSFLESFGQFPFVSFYCYFLNSEVRSAIRKRWHRWDKHSIRARV 420

QY 421 ARAMSIPTSPTRVSPHSIKOSTAV 444
DB 421 ARAMSIPTSPTRVSPHSIKOSTAV 444

RESULT 5
US-10-649-193-15
; Sequence 15, Application US/10649193
; Publication No. US20040039173A1
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: CRF Receptor(s)
; FILE REFERENCE: Salk1748
; CURRENT APPLICATION NUMBER: US/10/649,193
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; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/191,724
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/374,009
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/353,537
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-12-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US94/05908
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-05-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/110,286
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-08-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/079,320
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-06-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Homo sapiens
US-10-649-193-15

Query Match      100.0%; Score 2381; DB 4; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.7e-217;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGHQPQLRLVKALLLGLNPVSASLQDHCHESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGHQPQLRLVKALLLGLNPVSASLQDHCHESLSLASNISGLQCNASVDLIGTCWPRSPA 60

QY 61 GQLVVRPCAPFFGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHYHVAV 120
DB 61 GQLVVRPCAPFFGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHYHVAV 120

QY 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPQVRRSIRCLR 180
DB 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPQVRRSIRCLR 180

QY 181 NIHWNLISAFILRNATWFFVQLTMSPEVHQSNGVWCRLVTAAYNYFHVTFNPFMMFGECC 240
DB 181 NIHWNLISAFILRNATWFFVQLTMSPEVHQSNGVWCRLVTAAYNYFHVTFNPFMMFGECC 240

QY 241 YLHTAIVLTSTDRLRKWMFICIGWGPFPPIIIVAWAIGKLYDNEKCFGRPGVYTDYI 300
DB 241 YLHTAIVLTSTDRLRKWMFICIGWGPFPPIIIVAWAIGKLYDNEKCFGRPGVYTDYI 300

QY 301 YQGPMLVLVLLINFLFNIVIRILMTKLRASTTSETIQYKAVKATLVLLPLLGITYMLFF 360
DB 301 YQGPMLVLVLLINFLFNIVIRILMTKLRASTTSETIQYKAVKATLVLLPLLGITYMLFF 360

QY 361 VNPGEDEVSRVVIYFNPSFLESFGQFPFVSFYCYFLNSEVRSAIRKRWHRWDKHSIRARV 420
DB 361 VNPGEDEVSRVVIYFNPSFLESFGQFPFVSFYCYFLNSEVRSAIRKRWHRWDKHSIRARV 420

QY 421 ARAMSIPTSPTRVSPHSIKOSTAV 444
DB 421 ARAMSIPTSPTRVSPHSIKOSTAV 444

RESULT 6
US-10-292-798-708
; Sequence 708, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABEURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
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; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 708
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-708

Query Match 97.6%; Score 2324; DB 4; Length 447;
Best Local Similarity 99.8%; Pred. No. 4.6e-212;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 KALLLLGLNPVSASLQDQHCHESLSLASNISGLQCNASVDLIGTCWPRSPAGQLVVRPCPA 70
DB 14 RALLLLGLNPVSASLQDQHCHESLSLASNISGLQCNASVDLIGTCWPRSPAGQLVVRPCPA 73
QY 71 FFYGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHYHVAVIINYLGHCHIS 130
DB 74 FFYGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHYHVAVIINYLGHCHIS 133
QY 131 LVALLVAFVFLRLRPGCTHWGDAQALEVGAPWPGAPQVRRSIRCLNIIHMNLISA 190
DB 134 LVALLVAFVFLRLRPGCTHWGDAQALEVGAPWPGAPQVRRSIRCLNIIHMNLISA 193
QY 191 FILRNATFWVQLTMSPEVHQSNVGCRLVTAAYNFHVNTNPFWMFGECCYLHTAIVLTY 250
DB 194 FILRNATFWVQLTMSPEVHQSNVGCRLVTAAYNFHVNTNPFWMFGECCYLHTAIVLTY 253
QY 251 STDRLRKWPFICIGWGPVPPPIIVAMAIGKLYYDNEKCFGKRPGVYTDYIYQGPMLIVLL 310
DB 254 STDRLRKWPFICIGWGPVPPPIIVAMAIGKLYYDNEKCFGKRPGVYTDYIYQGPMLIVLL 313
QY 311 INFIFLNFVIRILMTKLRASTTSETTOYRKAVKATVLLPLLGITTYMLFPVNPGEDEVSR 370
DB 314 INFIFLNFVIRILMTKLRASTTSETTOYRKAVKATVLLPLLGITTYMLFPVNPGEDEVSR 373
QY 371 VFIYNSFLESFQGFVSVFYCFNLSEVRSARKEWHRWQDKHSIRARVARAWSIPTSP 430
DB 374 VFIYNSFLESFQGFVSVFYCFNLSEVRSARKEWHRWQDKHSIRARVARAWSIPTSP 433
QY 431 TRVSFHSIKQSTAV 444
DB 434 TRVSFHSIKQSTAV 447

RESULT 7
US-09-191-724-2
; Sequence 2, Application US/09191724
; Patent No. US20020055617A1
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; FILE REFERENCE: CRF Receptor(s)
; FILE REFERENCE: Salk1748
; CURRENT APPLICATION NUMBER: US/09/191,724
; EARLIER APPLICATION NUMBER: US 08/374,009
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: US 08/374,009
; EARLIER FILING DATE: 1995-01-17
; EARLIER APPLICATION NUMBER: US 08/353,537
; EARLIER FILING DATE: 1994-12-09
; EARLIER APPLICATION NUMBER: PCT/US94/05908
; EARLIER FILING DATE: 1993-05-25
; EARLIER APPLICATION NUMBER: US 08/110,286
; EARLIER FILING DATE: 1993-08-23
; EARLIER APPLICATION NUMBER: US 08/079,320
; EARLIER FILING DATE: 1993-06-18

; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-191-724-2

Query Match 91.8%; Score 2186.5; DB 3; Length 415;
Best Local Similarity 93.5%; Pred. No. 5e-199;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCHESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCHESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHYHVAV 120
DB 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHYHVAV 120
QY 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQALEVGAPWPGAPQVRRSIRCLR 180
DB 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQALEVGAPWPGAPQVRRSIRCLR 180
QY 181 NIHMNLISAFILRNATFWVQLTMSPEVHQSNVGCRLVTAAYNFHVNTNPFWMFGECC 240
DB 152 NIHMNLISAFILRNATFWVQLTMSPEVHQSNVGCRLVTAAYNFHVNTNPFWMFGECC 211
QY 241 YLHTAIVLTYSTDRLRKWPFICIGWGPVPPPIIVAMAIGKLYYDNEKCFGKRPGVYTDYI 300
DB 212 YLHTAIVLTYSTDRLRKWPFICIGWGPVPPPIIVAMAIGKLYYDNEKCFGKRPGVYTDYI 271
QY 301 YQGPMLIVLLINFIFLNFVIRILMTKLRASTTSETTOYRKAVKATVLLPLLGITTYMLFF 360
DB 272 YQGPMLIVLLINFIFLNFVIRILMTKLRASTTSETTOYRKAVKATVLLPLLGITTYMLFF 331
QY 361 VNPGEDEVSRVFIYNSFLESFQGFVSVFYCFNLSEVRSARKEWHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVFIYNSFLESFQGFVSVFYCFNLSEVRSARKEWHRWQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSPHSIKQSTAV 444
DB 392 ARAMSIPTSPTRVSPHSIKQSTAV 415

RESULT 8
US-09-799-978-2
; Sequence 2, Application US/09799978
; Publication No. US20030165807A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or
; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors
; FILE REFERENCE: 8448
; CURRENT APPLICATION NUMBER: US/09/799,978
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-799-978-2

Query Match 91.8%; Score 2186.5; DB 3; Length 415;
Best Local Similarity 93.5%; Pred. No. 5e-199;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCHESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCHESLSLASNISGLQCNASVDLIGTCWPRSPA 60

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QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHHVAV 120
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Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHHVAV 120
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|
QY 121 IINYLGHCSLVALLVAFVLFRLRPGCTHWGDAQDGALEVGAPWSGAPQVRRSIRCLR 180
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Db 121 IINYLGHCSLVALLVAFVLFRLR-----RSIRCLR 151
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|
QY 181 NIHWNLISAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWMFGECC 240
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|
|
Db 152 NIHWNLISAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWMFGECC 211
|
|
|
QY 241 YLHTAIVLTSTDRLRKMPICIGWGPVPIIIVAWAIGKLYYDNEKCFGRPGVYTDYI 300
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|
Db 212 YLHTAIVLTSTDRLRKMPICIGWGPVPIIIVAWAIGKLYYDNEKCFGRPGVYTDYI 271
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|
|
QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITMYLFF 360
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|
Db 272 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITMYLFF 331
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|
|
QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRQDKHSIRARV 420
|
|
|
Db 332 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRQDKHSIRARV 391
|
|
|
QY 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444
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Db 392 ARAMSIPTSPTRVSVFHSIKQSTAV 415
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|
RESULT 9
US-09-799-978-4
; Sequence 4, Application US/09799978
; Publication No. US20030165807A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or
; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors
; FILE REFERENCE: 8448
; CURRENT APPLICATION NUMBER: US/09/799,978
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-978-4
Query Match 91.8%; Score 2186.5; DB 3; Length 415;
Best Local Similarity 93.5%; Pred. No. 5e-199;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY 1 MGGHPQLRLVKALLLGLNLPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
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Db 1 MGGHPQLRLVKALLLGLNLPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
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QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHHVAV 120
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Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHHVAV 120
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QY 121 IINYLGHCSLVALLVAFVLFRLRPGCTHWGDAQDGALEVGAPWSGAPQVRRSIRCLR 180
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Db 121 IINYLGHCSLVALLVAFVLFRLR-----RSIRCLR 151
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QY 181 NIHWNLISAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWMFGECC 240
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Db 152 NIHWNLISAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWMFGECC 211
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QY 241 YLHTAIVLTSTDRLRKMPICIGWGPVPIIIVAWAIGKLYYDNEKCFGRPGVYTDYI 300
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Db 212 YLHTAIVLTSTDRLRKMPICIGWGPVPIIIVAWAIGKLYYDNEKCFGRPGVYTDYI 271
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QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITMYLFF 360
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Db 272 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITMYLFF 331
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QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRQDKHSIRARV 420
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Db 332 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRQDKHSIRARV 391
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|
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QY 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444
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Db 392 ARAMSIPTSPTRVSVFHSIKQSTAV 415
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Db 212 YLHTAIVLTSTDRLRKMPICIGWGPVPIIIVAWAIGKLYYDNEKCFGRPGVYTDYI 271
QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITMYLFF 360
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Db 272 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITMYLFF 331
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QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRQDKHSIRARV 420
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Db 332 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRQDKHSIRARV 391
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|
QY 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444
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|
Db 392 ARAMSIPTSPTRVSVFHSIKQSTAV 415
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|
RESULT 10
US-10-242-822B-1
; Sequence 1, Application US/10242822B
; Publication No. US20030113799A1
; GENERAL INFORMATION:
; APPLICANT: Pisarski, Alexander
; APPLICANT: Slominski, Andrzej
; TITLE OF INVENTION: Variants of Corticotropin Releasing Hormone
; TITLE OF INVENTION: Receptor Type 1 and Uses Thereof
; FILE REFERENCE: D6420
; CURRENT APPLICATION NUMBER: US/10/242,822B
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/322,195
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 1
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: amino acid sequence of human CRH-R1 alpha
; OTHER INFORMATION: Gene: GenBank Accession No. US20030113799A1 L23332
US-10-242-822B-1
Query Match 91.8%; Score 2186.5; DB 4; Length 415;
Best Local Similarity 93.5%; Pred. No. 5e-199;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY 1 MGGHPQLRLVKALLLGLNLPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
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Db 1 MGGHPQLRLVKALLLGLNLPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
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QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHHVAV 120
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Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHHVAV 120
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|
QY 121 IINYLGHCSLVALLVAFVLFRLRPGCTHWGDAQDGALEVGAPWSGAPQVRRSIRCLR 180
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Db 121 IINYLGHCSLVALLVAFVLFRLR-----RSIRCLR 151
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QY 181 NIHWNLISAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWMFGECC 240
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Db 152 NIHWNLISAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWMFGECC 211
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QY 241 YLHTAIVLTSTDRLRKMPICIGWGPVPIIIVAWAIGKLYYDNEKCFGRPGVYTDYI 300
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Db 212 YLHTAIVLTSTDRLRKMPICIGWGPVPIIIVAWAIGKLYYDNEKCFGRPGVYTDYI 271
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QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITMYLFF 360
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|
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Db 272 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITMYLFF 331
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|
|
QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRQDKHSIRARV 420
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|
|
Db 332 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRQDKHSIRARV 391
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|
QY 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444
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|
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Db 392 ARAMSIPTSPTRVSPHSIKQSTAV 415

RESULT 11

US-10-649-193-2

; Sequence 2, Application US/10649193

; Publication No. US20040039173A1

; GENERAL INFORMATION:

; APPLICANT: Perrin, Marilyn H.

; APPLICANT: Chen, Ruoping A.

; APPLICANT: Lewis, Kathy A.

; APPLICANT: Vale Jr., Wylie W.

; APPLICANT: Donaldson, Cynthia J.

; APPLICANT: Sawchenko, Paul

; TITLE OF INVENTION: Cloning and Recombinant Production of

; TITLE OF INVENTION: CRF Receptor(s)

; FILE REFERENCE: Salk1748

; CURRENT APPLICATION NUMBER: US/10/649,193

; CURRENT FILING DATE: 2003-08-26

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/191,724

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-12

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/374,009

; PRIOR FILING DATE: EARLIER FILING DATE: 1995-01-17

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/353,537

; PRIOR FILING DATE: EARLIER FILING DATE: 1994-12-09

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US94/05908

; PRIOR FILING DATE: EARLIER FILING DATE: 1993-05-25

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/110,286

; PRIOR FILING DATE: EARLIER FILING DATE: 1993-08-23

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/079,320

; PRIOR FILING DATE: EARLIER FILING DATE: 1993-06-18

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 415

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-649-193-2

Query Match

Best Local Similarity 91.8%; Score 2186.5; DB 4; Length 415;

Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

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QY 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
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Db 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
   |||||

QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNTSECOEILNEEKSKVHYHVAV 120
   |||||
Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNTSECOEILNEEKSKVHYHVAV 120
   |||||

QY 121 IINYLGHCSLVALLVAFVFLRLRPGCTHWGDQADGALVGPWPGAPQVRRSTRCLR 180
   |||||
Db 121 IINYLGHCSLVALLVAFVFLRLRPGCTHWGDQADGALVGPWPGAPQVRRSTRCLR 180
   |||||

QY 181 NIHNWNLISAFILRNATFVQVLTMSPEVHQSVNGWCRLVTAAYNYFHVTFNPFWMFEGGC 240
   |||||
Db 152 NIHNWNLISAFILRNATFVQVLTMSPEVHQSVNGWCRLVTAAYNYFHVTFNPFWMFEGGC 211
   |||||

QY 241 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCFKRPVGYTDYI 300
   |||||
Db 212 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCFKRPVGYTDYI 271
   |||||

QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASSTSETIOYRKAVKATLVLLPLGITVMLPFF 360
   |||||
Db 272 YQGPMLVLLINFIPLFNIVRIILMTKLRASSTSETIOYRKAVKATLVLLPLGITVMLPFF 331
   |||||

QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
   |||||
Db 332 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 391
   |||||

QY 421 ARAMSIPTSPTRVSPHSIKQSTAV 444
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Db 392 ARAMSIPTSPTRVSPHSIKQSTAV 415

RESULT 12

US-10-649-852-2

; Sequence 2, Application US/10649852

; Publication No. US20040101911A1

; GENERAL INFORMATION:

; APPLICANT: The Procter & Gamble Company

; APPLICANT: Isfort, Robert

; APPLICANT: Sheldon, Russell

; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F

; TITLE OF INVENTION: Using Corticotropin Releasing Factor Receptors

; FILE REFERENCE: 8448R

; CURRENT APPLICATION NUMBER: US/10/649,852

; CURRENT FILING DATE: 2003-08-27

; PRIOR APPLICATION NUMBER: US 09/799,978

; PRIOR FILING DATE: 2001-03-06

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 415

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-649-852-2

Query Match 91.8%; Score 2186.5; DB 4; Length 415;

Best Local Similarity 93.5%; Pred. No. 5e-199; 0; Mismatches 0; Indels 29; Gaps 1;

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QY 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
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Db 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
   |||||

QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNTSECOEILNEEKSKVHYHVAV 120
   |||||
Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNTSECOEILNEEKSKVHYHVAV 120
   |||||

QY 121 IINYLGHCSLVALLVAFVFLRLRPGCTHWGDQADGALVGPWPGAPQVRRSTRCLR 180
   |||||
Db 121 IINYLGHCSLVALLVAFVFLRLRPGCTHWGDQADGALVGPWPGAPQVRRSTRCLR 180
   |||||

QY 181 NIHNWNLISAFILRNATFVQVLTMSPEVHQSVNGWCRLVTAAYNYFHVTFNPFWMFEGGC 240
   |||||
Db 152 NIHNWNLISAFILRNATFVQVLTMSPEVHQSVNGWCRLVTAAYNYFHVTFNPFWMFEGGC 211
   |||||

QY 241 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCFKRPVGYTDYI 300
   |||||
Db 212 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCFKRPVGYTDYI 271
   |||||

QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASSTSETIOYRKAVKATLVLLPLGITVMLPFF 360
   |||||
Db 272 YQGPMLVLLINFIPLFNIVRIILMTKLRASSTSETIOYRKAVKATLVLLPLGITVMLPFF 331
   |||||

QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
   |||||
Db 332 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 391
   |||||

QY 421 ARAMSIPTSPTRVSPHSIKQSTAV 444
   |||||
Db 392 ARAMSIPTSPTRVSPHSIKQSTAV 415
   |||||

RESULT 13
US-10-649-852-4
; Sequence 4, Application US/10649852
; Publication No. US20040101911A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F
; TITLE OF INVENTION: Using Corticotropin Releasing Factor Receptors
```


FILE REFERENCE: 8448R
CURRENT APPLICATION NUMBER: US/10/649,852
PRIOR FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 09/799,978
PRIOR FILING DATE: 2001-03-06
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 415
TYPE: PRT
ORGANISM: Homo sapiens
US-10-649-852-4

Query Match 91.8%; Score 2186.5; DB 4; Length 415;
Best Local Similarity 93.5%; Pred. No. 5e-199; Indels 29; Gaps 1;
Matches 415; Conservative 0; Mismatches 0

QY 1 MCGHPQLRLVKALLLGLNPNVSLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MCGHPQLRLVKALLLGLNPNVSLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60

QY 61 GOLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKSKVHYHVA 120
DB 61 GOLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKSKVHYHVA 120

QY 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDALEVGAPWSGAPFQVRRSTRCLR 180
DB 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDALEVGAPWSGAPFQVRRSTRCLR 180

QY 181 NIHNWNLISAFILRNATFVQVLTMSPEVHQSNGVNCRLVTAAYNYFHVNTNPFMMFGECC 240
DB 152 NIHNWNLISAFILRNATFVQVLTMSPEVHQSNGVNCRLVTAAYNYFHVNTNPFMMFGECC 211

QY 241 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIIVAMAIGKLYYDNEKCFKRGVYTDYI 300
DB 212 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIIVAMAIGKLYYDNEKCFKRGVYTDYI 271

QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIYQYKAVKATVLLPLGITMFLFF 360
DB 272 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIYQYKAVKATVLLPLGITMFLFF 331

QY 361 VNPGEDEVSRVPIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVPIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 391

QY 421 ARAMSIPTSPTRVSHSIKQSTAV 444
DB 392 ARAMSIPTSPTRVSHSIKQSTAV 415

RESULT 14
US-10-450-097-14
Sequence 14, Application US/10450097
Publication No. US20040110252A1
GENERAL INFORMATION:
APPLICANT: Septegen Ltd
TITLE OF INVENTION: Yeast-Based Assay
FILE REFERENCE: DE/p/01948PCT
CURRENT APPLICATION NUMBER: US/10/450,097
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: GB 0030038.4
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 415
TYPE: PRT
ORGANISM: Homo sapiens
US-10-450-097-14

Query Match 91.8%; Score 2186.5; DB 4; Length 415;
Best Local Similarity 93.5%; Pred. No. 5e-199; Indels 29; Gaps 1;
Matches 415; Conservative 0; Mismatches 0

QY 1 MCGHPQLRLVKALLLGLNPNVSLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MCGHPQLRLVKALLLGLNPNVSLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60

QY 61 GOLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKSKVHYHVA 120
DB 61 GOLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKSKVHYHVA 120

QY 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDALEVGAPWSGAPFQVRRSTRCLR 180
DB 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDALEVGAPWSGAPFQVRRSTRCLR 180

QY 181 NIHNWNLISAFILRNATFVQVLTMSPEVHQSNGVNCRLVTAAYNYFHVNTNPFMMFGECC 240
DB 152 NIHNWNLISAFILRNATFVQVLTMSPEVHQSNGVNCRLVTAAYNYFHVNTNPFMMFGECC 211

QY 241 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIIVAMAIGKLYYDNEKCFKRGVYTDYI 300
DB 212 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIIVAMAIGKLYYDNEKCFKRGVYTDYI 271

QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIYQYKAVKATVLLPLGITMFLFF 360
DB 272 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIYQYKAVKATVLLPLGITMFLFF 331

QY 361 VNPGEDEVSRVPIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVPIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 391

QY 421 ARAMSIPTSPTRVSHSIKQSTAV 444
DB 392 ARAMSIPTSPTRVSHSIKQSTAV 415

RESULT 15
US-09-826-509-483
Sequence 483, Application US/09826509
Publication No. US20030204073A1
GENERAL INFORMATION:
APPLICANT: Lehmann-Brunnsma, Karin
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-lin
TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
FILE REFERENCE: AREN-207
CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 483
LENGTH: 415
TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-509-483

Query Match 91.6%; Score 2180.5; DB 3; Length 415;
Best Local Similarity 93.2%; Pred. No. 1.9e-198; Indels 29; Gaps 1;
Matches 414; Conservative 0; Mismatches 1

QY 1 MCGHPQLRLVKALLLGLNPNVSLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MCGHPQLRLVKALLLGLNPNVSLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60

QY 61 GOLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKSKVHYHVA 120
DB 61 GOLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKSKVHYHVA 120

QY 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDALEVGAPWSGAPFQVRRSTRCLR 180
DB 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDALEVGAPWSGAPFQVRRSTRCLR 180

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Db 121 IINYLGHICISLVALVAFVLFLRL-----RSIRCLR 151
QY 181 NIITHMNLISAFILRNATWVVQLTMSPEVHQSNVGMCRLVTAAYNYFHVNTNFFWMEGEC 240
Db 152 NIITHMNLISAFILRNATWVVQLTMSPEVHQSNVGMCRLVTAAYNYFHVNTNFFWMEGEC 211
QY 241 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCMFGKRPGVYTDYI 300
Db 212 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCMFGKRPGVYTDYI 271
QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIOYRKAVKATVLLPLLGITTMLFF 360
Db 272 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIOYRKAVKAPVLLPLLGITTMLFF 331
QY 361 VNPGEDEVSRVVIYFNSPLESPQGFVSVFYCFLNSEVRSATRKWHRWQDKHSIRARV 420
Db 332 VNPGEDEVSRVVIYFNSPLESPQGFVSVFYCFLNSEVRSATRKWHRWQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSPHSIKQSTAV 444
Db 392 ARAMSIPTSPTRVSPHSIKQSTAV 415
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Search completed: March 16, 2006, 17:24:47
Job time : 170 secs

Result No.	Query			Description		
	Score	Match	Length	ID	DB	
1	498.5	20.9	273	7	US-11-206-587-34	Sequence 34, Appl
2	478	20.1	463	6	US-10-501-411A-341	Sequence 341, Appl
3	459.5	19.3	438	7	US-11-090-439-29	Sequence 29, Appl
4	459.5	19.3	438	7	US-11-090-439-31	Sequence 31, Appl
5	209	8.8	910	7	US-11-206-587-17	Sequence 17, Appl
6	207.5	8.7	742	7	US-11-127-877-43	Sequence 43, Appl
7	207.5	8.7	765	6	US-10-821-234-1164	Sequence 1164, Ap
8	205	8.6	690	6	US-10-131-826A-306	Sequence 306, App
9	205	8.6	690	6	US-10-973-115B-306	Sequence 306, App
10	189.5	8.0	797	7	US-11-241-956-4	Sequence 4, Appl
11	182	7.6	693	6	US-10-131-826A-406	Sequence 406, App
12	182	7.6	693	6	US-10-973-115B-406	Sequence 406, App
13	166	7.0	549	7	US-11-241-956-7	Sequence 7, Appl
14	165	6.9	2923	7	US-11-200-822-3	Sequence 3, Appl
15	163	6.8	578	7	US-11-241-956-2	Sequence 2, Appl
16	156.5	6.6	565	7	US-11-080-991-100	Sequence 100, App
17	98.5	4.1	380	6	US-10-330-773-443	Sequence 443, App
18	98.5	4.1	920	7	US-11-072-512-2574	Sequence 2574, Ap
19	97.5	4.1	410	7	US-11-096-568A-7537	Sequence 7537, Ap
20	97.5	4.1	409	7	US-11-067-884-8	Sequence 8, Appl
21	97.5	4.1	432	7	US-11-087-099-4608	Sequence 4608, Ap
22	97.5	4.1	432	7	US-11-096-568A-7536	Sequence 7536, Ap
23	97	4.1	342	7	US-11-174-751-19	Sequence 19, Appl
24	97	4.1	358	6	US-10-055-877-177	Sequence 177, App
25	94.5	4.0	358	7	US-11-174-819-17	Sequence 17, Appl

QY 285 EK-CWFGKRGVYTDYIYQGMILVLLINFIPLFNIVRILMTKLRAST-----TSETIQYR 339
Db 150 EGCWLSNDTNGFWMIKGPILLIILVFIPIFINILRIILVQKLRIIDSLSPQIGETDQYR 209
QY 340 K-AVKATLVLLPLGLTYMLFFVNPQDE--VSRVVFYFNSFLESFGQFVSVFYCF 394
Db 210 KGLRVKSTLLPLGLTWILFLFAP-EDQSQGLSLVFLYFLIILNSPQGFVAVLYCF 268
QY 395 LNSEV 399
Db 269 LNSEV 273

RESULT 2
US-10-501-411A-341
; Sequence 341, Application US/10501411A
; Publication No. US20060014678A1
; GENERAL INFORMATION:
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolm
; APPLICANT: Bulter, Andrew
; APPLICANT: Bloom, Stephen Robert
; APPLICANT: Small, Caroline Jane
; APPLICANT: Batterham, Rachel Louise
; APPLICANT: Ghatel, Mohammad Ali
; TITLE OF INVENTION: Modification of Feeding Behavior Using PYY and GLP-1
; FILE REFERENCE: AI 9248US
; CURRENT APPLICATION NUMBER: US/10/501,411A
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: PCT/GB03/00062
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: PCT/US02/31944
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: 60/392,109
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0200507.2
; PRIOR FILING DATE: 2002-01-10
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 341
; LENGTH: 463
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-501-411A-341

Query Match 20.1%; Score 478; DB 6; Length 463;
Best Local Similarity 28.7%; Pred. No. 1.4e-36;
Matches 139; Conservative 74; Mismatches 172; Indels 100; Gaps 20;

QY 1 MCGHP-QLRVKAALLLGL-----NPVSASLQ-----DQHCSLSLASN---I 39
Db 1 MAGAPGLRL--ALLLLGMVGRAGRPQPGATVSLMETVQKRYRQCQR-SLTEDPPPPA 57
QY 40 SGIQCNASVDLIGTCWPRSPAGLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVN- 98
Db 58 TDLFCNRTFDEY-ACHWDEPGSFVANVSCPWYLPWASSVPGQHVYFCTAGLWLOKDNS 116
QY 99 -----YSEQEITLNEKSKVHYHVAVINI-LGHCISLVALLVAFVFLRLRPGCTHW 151
Db 117 SLPWRDLSECEKRGERSPEQLFLYIITVGVYALSPFSAIVIASAILLGF----- 169
QY 152 GDQADGALEVGAPWVGAPQVRSISCLRNIIHNLISAFILRNATWVVVOLT----- 205
Db 170 -----RHLHCTRYNIHNLIFASFILRALSVFINDAALKWMYST 207
QY 206 SPEVHQSNGW-----CRLVTAAYNYFHTNFFMMFGEGCYLHTAIVLITYSTDR 254
Db 208 AAQHQH----WQGLLSYQDSLSCLRVLLMQYCAANYWLLAVEGYLYLTLLAFVSFE- 262
QY 255 LRKWF-----ICITGWGPPFIIVAWATGKLYDNEKCFWGRKPGVYTDYIYQGMILVLLI 311
Db 263 --QWIFRLYVSGWGPVLLFVVPWGVKLYEDECW-TRNSNNMYWLIIRLPIILFAIGV 319

QY 312 NFIFLFNIVRILMTKLRASTSETIOYRKAVKATLVLLPLGLTYMLF-PVNPGEDEVSR 370
Db 320 NFIFVRVICIVSVKUKANLMCKTDIKCLRAKSTLLIPLLGTHFVIFAPV---MDEHAR 376
QY 371 VFIYFNSFLE-----SFQGFVSVFYCFNLSEVRSAIRKRWHRW--QDKHSIRARVARAM 424
Db 377 GTLRFIKLFTLSFTSFQGLWVAILYCFVNVVQLEFRKSWERWRLHHLHIQDSSMKPL 436
QY 425 SIPTS 429
Db 437 KCPTS 441

RESULT 3
US-11-090-439-29
; Sequence 29, Application US/11090439
; Publication No. US20050266442A1
; GENERAL INFORMATION:
; APPLICANT: Squillace, Rachel
; APPLICANT: Weiner, Michael P.
; TITLE OF INVENTION: Immortalized Human Tuberos Sclerosis Null
; FILE REFERENCE: 24318-502
; CURRENT APPLICATION NUMBER: US/11/090,439
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/556,344
; PRIOR FILING DATE: 2004-03-25
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-439-29

Query Match 19.3%; Score 459.5; DB 7; Length 438;
Best Local Similarity 28.2%; Pred. No. 6.8e-35;
Matches 118; Conservative 75; Mismatches 161; Indels 65; Gaps 13;

QY 4 HPQLRLVKALLLGLNPNVSASLQDQHCSLSLASNISGLQCNASVDLIGTCWPRSPAGQL 63
Db 22 HPECRF-----HLEIQBEETKCAELLRSQTEKHKACSGVWDNI-TCWPRANVGET 70
QY 64 VVRPCPAPFYGVRYNTNNGYRECLANGSWAARVNVSECEILNEKSKVHYHVAVINI 123
Db 71 VTPCPKVFENF-YSKAGNISKNCTSDGWSSETFPDFVADGCGYSDPEDESKITFYIILVKAI 129
QY 124 Y-LGHCISLVALLVAFVFLRLRPGCTHWGDQADGALEVGAPWVGAPFVRSIRCLRNI 182
Db 130 YILGYSVLSMLSATGSIIL-----C-----LFRKLHCTRYN 160
QY 183 IHNLISAFILRNATWVVVOLTMSPEVHQSNGV-----W-CRLVTAAYNYFHTV 230
Db 161 IHLNLFSLFILR-----AISVLKDDVLYSSSTGLHCPDPSPSSWGCKLSLVLQYCINA 215
QY 231 NFFWMPGEGCYLHTAIVLITYSTDRLKNMFPICIGWGPPIIVANAIGKLYDNEKCFW 290
Db 216 NFFWLLAVEGLYLTLLVAVMLPPRR-FLAYLLIGMGLPTVCIGAMTAARLYLEDTCGMDT 274
QY 291 KRPGVYTDYIYQGMILVLLINFIPLFNIVRILMTKLRASTT--SETIOYRKAVKATLV 348
Db 275 NDHSV-PWVIRIPILISIIIVNFVLFISIIRILLQKLTSPDVGNDQSQYKRLAKSTLLL 333
QY 349 LPPLGLTYMLFFVNPGEDEVSRVFIYFNSFLESFGQFVSVFYCFNLSEVRSAIRKRW 407
Db 334 IPLFGVHYNVFAVFP--ISISSKYQLPELCLGSGFGLVAVLYCFNLSEVQCELCRKN 390

RESULT 4
US-11-090-439-31
; Sequence 31, Application US/11090439
; Publication No. US20050266442A1

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; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 910
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-206-587-17

Query Match      8.8%; Score 209; DB 7; Length 910;
Best Local Similarity 23.4%; Pred. No. 2.7e-11;
Matches 74; Conservative 62; Mismatches 122; Indels 58; Gaps 14;

QY 122 INVLGHCISIVALLVAFV--LFLRLRPGCTHGGDQADGALEVPAGWSGAPFQVRRS-IR 177
DB 588 ITVVGIGSIGSDILCLITALEP-----WK-----QIKKSQTS 620

QY 178 CLRNIIHMLNLSAFILRNATVFFVQVLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWMFG 237
DB 621 HTRICVMNIALSLIAD-VVFIVGATVDTVPNSGV--CTAAVFFTHFFVLSLFFWMLM 677

QY 238 EGYLHTAIVLT--STDRLRKWMFTICIGVGPPI-IVAWAI---GKLYDNEKCKWPGK 291
DB 678 LGTLLAYRIILVFHRMAQLMVAVGCLGYGCPILISVITIAVTPSNTYKRKDVCLNW 737

QY 292 RGVYTDYIQGPMLVLLNIFLFINVILMTKLRASSTSIQ-----YKAVKAT 345
DB 738 SNGGKPLPAFVPPALAIVANFV---VLLVLTKLWRPVGRLSRDDKATIIRVGKSL 793

QY 346 LVLLPLLGITMYLFFVNPGBDEYSRVVFIYFNSPLSFSGFQFFVSVFCFLNSEVRSAIRK 405
DB 794 LIITPLILGLTWG-FGIGTIVDSQNLAWHVF-ALLNAAFQFFILCFGLILDSKLRQLLEN 851

QY 406 R-----WHRWDQKHS 415
DB 852 KLSALSSWKQTEKQNS 867

RESULT 6
US-11-127-877-43
; Sequence 43, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: F27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 43
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-43

Query Match      8.7%; Score 207.5; DB 7; Length 742;
Best Local Similarity 26.9%; Pred. No. 3e-11;
Matches 89; Conservative 51; Mismatches 128; Indels 63; Gaps 18;

QY 90 NGSWAARVNYSEQEILNBEKSKSVHYV-----AVIINYLGHICISLVALLVAFVFLRLR 145
DB 427 NGSTTCOCSHLSFALL-----MAHYDVEDWKLTLITRVGLALSFLCILLCILTLFLVR 480

QY 146 PGCTHGGDQADGALEVPAGWSGAPFQVRRSIRCLRNIIHNL-ISAFILRNATVFFVQVLT 204

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Db 481 P-----IQSRTTIHLHCICLVF--GSTIFLAGI- 508
QY 205 MSPEVHQSNGM-CRLVTAAYNYFHTNPFWMFEGCYLHTAIVLYSTDR-L-RKMWFIC 262
Db 509 ---ENEGGQVGLRCRLVAGLLHYCFLAACWMSLEGLHYFLVVRVFOQGLSTRWLCI- 564
QY 263 IGMGVFPPII-VAMAI-GKLYDNEKCMFKRGVYTDYIQGPMILVLLIN-FIFLNI 319
Db 565 IGVGPVLLIVGSAIYSKGYGRPCWLDPEQGLWSFL--GPVTFILCNVAVFTTV 622
QY 320 VRILMTKLRASTTSETIQRVKAVKATLV-LPLLGITYM--LFFVNPGEDEVSRVFIYP 376
Db 623 WKLTQKFSINPDMMKKLKRALTITAIQLFLGCTWVGLFIF----DDRS-LVLTIV 677
QY 377 NSPLESFOGFVSVFCFLNSEVRSRAIRKW 407
Db 678 FTILNCLQAGFLYLLHCLLNKKVREYRK-W 707

RESULT 7

US-10-821-234-1164
; Sequence 1164, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1164
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1164

Query Match 8.7%; Score 207.5; DB 6; Length 765;
Best Local Similarity 26.9%; Pred. No. 3.1e-11;
Matches 89; Conservative 51; Mismatches 128; Indels 63; Gaps 18;

QY 90 NGSWAARVNSYEQEILNEBKSKVHYV-----AVIINYLGHICISLVALLVAFVFLRLR 145
Db 450 NGSTTCQCHLSFAIL-----MAHYDVEDWKLTLITRVGLALSFLCLLCILTELLVR 503
QY 146 PGCTHWGDQADGALEVGAPWSPGAPQVRSIRCLRNIIHWNL-ISAFILRNATWFWVQLT 204
Db 504 P-----IQSRTTIHLHCICLVF--GSTIFLAGI- 531
QY 205 MSPEVHQSNGM-CRLVTAAYNYFHTNPFWMFEGCYLHTAIVLYSTDR-L-RKMWFIC 262
Db 532 ---ENEGGQVGLRCRLVAGLLHYCFLAACWMSLEGLHYFLVVRVFOQGLSTRWLCI- 587
QY 263 IGMGVFPPII-VAMAI-GKLYDNEKCMFKRGVYTDYIQGPMILVLLIN-FIFLNI 319
Db 588 IGVGPVLLIVGSAIYSKGYGRPCWLDPEQGLWSFL--GPVTFILCNVAVFTTV 645
QY 320 VRILMTKLRASTTSETIQRVKAVKATLV-LPLLGITYM--LFFVNPGEDEVSRVFIYP 376
Db 646 WKLTQKFSINPDMMKKLKRALTITAIQLFLGCTWVGLFIF----DDRS-LVLTIV 700
QY 377 NSPLESFOGFVSVFCFLNSEVRSRAIRKW 407
Db 701 FTILNCLQAGFLYLLHCLLNKKVREYRK-W 730

RESULT 8

US-10-131-826A-306

; Sequence 306, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 306
; NUMBER OF SEQ ID NOS: 550
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-306

Query Match 8.6%; Score 205; DB 6; Length 690;
Best Local Similarity 23.2%; Pred. No. 4.7e-11;
Matches 86; Conservative 54; Mismatches 135; Indels 96; Gaps 17;
QY 73 YGVRYNTNNGVRECLA-----NGSWAA---RVNSYEQEILNEBKKS-----KVH 115
Db 355 FTLSHRKVTDYRSLCAFWNSPDTMNGSWSEGCGLTYS-----NETHTSRCNHLTH 408
QY 116 -----YHVAIINYLGHICISLVALLVAFVFLRLRPGCTHWGDQADGALE 160
Db 409 FAILSSGPSIGIKDYNILTRITQIGIISLICIAICTF----- 449
QY 161 VGAPSGAPQVRSIRCLRNIIHWNLISAFILRNATWFWVQLTMSPEVHQSNGVWCRIV 220
Db 450 ----WFSS-----BIQSTRFTIHKNLCCSLFAELVFLVGINT-----NTNKLFCsii 493
QY 221 TAAVNYFHTNPFWMFEGCYLHTAIV-LTYSTDRLRKMWFICIGWGVFPPIIV---AWA 276
Db 494 AGLLHYFFLAAPAWMCIEGIIHLIVGVGVYINKGFLHKNFYI---FGYLSPAVVVGFSA 550

QY 277 IGKLYDNEK-CWFGKRPQVYTDYIYOGPMILVLLNFIPLFNIVRILMTKLAESTTSET 335
DB 551 LGVRYGTGTTKVCWLSTENNFIWFSFI--GPACLIILVN-LIAFGVLIYKVPFRHTAGLKPEV 607
QY 336 IQY---RKAVKATLVLPLLGITY---MLPFVNPGEDESVRVVFIYFNSFLESFQGFVFS 389
DB 608 SCFENIRSCARGALALLFLGTTWIFGVHLVHVH-----ASVVTAYLFTVSNAPQGMFIF 661
QY 390 VFYCFNLSEVR 400
DB 662 LFLCVLSRKIQ 672

RESULT 9

US-10-973-115B-306

; Sequence 306, Application US/10973115B

; Publication No. US20060040351A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: Deforge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING

; FILE REFERENCE: 39870-3330R1C300C1

; CURRENT APPLICATION NUMBER: US/10/973,115B

; CURRENT FILING DATE: 2004-10-22

; PRIOR APPLICATION NUMBER: US 10/145,747

; PRIOR FILING DATE: 2002-05-14

; PRIOR APPLICATION NUMBER: US 10/028,072

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: PCT/US00/32678

; PRIOR FILING DATE: 2000-12-01

; PRIOR APPLICATION NUMBER: US 09/581,742

; PRIOR FILING DATE: 2000-06-16

; PRIOR APPLICATION NUMBER: PCT/US00/05746

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: US 60/135,736

; PRIOR FILING DATE: 1999-05-25

; PRIOR APPLICATION NUMBER: US 60/123,090

; PRIOR FILING DATE: 1999-03-05

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 306

; LENGTH: 690

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-973-115B-306

Query Match 8.6%; Score 205; DB 6; Length 690;

Best Local Similarity 23.2%; Pred. No. 4.7e-11;

Matches 86; Conservative 54; Mismatches 135; Indels 96; Gaps 17;

QY 73 YGVRYNTNNGYRECLA-----NGSWAA-----RVNYSECQILNEEKKS-----KVH 115

DB 355 FTLSHRKVTDRYSLCAFWNVPDTMGNSWSEGCETYS-----NETHTSCRNHLTH 408

QY 116 -----YHVAIIVNLHCISIVALLVAVFLRLRPGCTHWGDAQDALE 160

DB 409 FAILMSGSPSIGINDKYNILRITQIGIISICLAICITFT----- 449

QY 161 VGAPSGAPQVRRSIRCLRNIIHWNLIISAFILRNATFWVQLTMSPEVHQSNVGHCLV 220
DB 450 -----NFFS-----EQSTRTTIHKNLCCSLFLAELVFLVGINT-----NTNKLFCSEII 493
QY 221 TAAVNYFHTNPFWMFEGEGCYLHTAIV-LTYSSTRDLRKWMFICIGWGVPPPIIV---AWA 276
DB 494 AGLLHFFFLAAFAWMCIEGHLHLVIVGVYINNGFLHKNFYI---FGYLSPAVVVGFSAA 550
QY 277 IGKLYDNEK-CWFGKRPQVYTDYIYOGPMILVLLNFIPLFNIVRILMTKLAESTTSET 335
DB 551 LGVRYGTGTTKVCWLSTENNFIWFSFI--GPACLIILVN-LIAFGVLIYKVPFRHTAGLKPEV 607
QY 336 IQY---RKAVKATLVLPLLGITY---MLPFVNPGEDESVRVVFIYFNSFLESFQGFVFS 389
DB 608 SCFENIRSCARGALALLFLGTTWIFGVHLVHVH-----ASVVTAYLFTVSNAPQGMFIF 661
QY 390 VFYCFNLSEVR 400
DB 662 LFLCVLSRKIQ 672

RESULT 10

US-11-241-956-4

; Sequence 4, Application US/11241956

; Publication No. US20060024792A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS INC.; BAUGHN, Mariah R.;

; APPLICANT: GANDHI, Ameena R.; CHAWLA, Navinder K.;

; APPLICANT: RAMKUMAR, Jayalaxmi; TRIBOULEY, Catherine M.;

; APPLICANT: THORNTON, Michael B.; KALLICK, Deborah A.;

; APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;

; APPLICANT: BURFORD, Neil; KHAN, Farrah A.;

; APPLICANT: YUE, Henry; LU, Yan;

; APPLICANT: ARVIZU, Chandra S.; ROOPA, Reddy M.;

; APPLICANT: NGUYEN, Daniel B.; LEE, Ernestine A.;

; APPLICANT: LU, Dying Aina M.; ISON, Craig H.;

; APPLICANT: WALSH, Roderick T.; POLICKY, Jennifer L.

; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS

; FILE REFERENCE: PI-0236 USN

; CURRENT APPLICATION NUMBER: US/11/241,956

; CURRENT FILING DATE: 2005-10-04

; PRIOR APPLICATION NUMBER: US/10/398,036

; PRIOR FILING DATE: 2003-03-28

; PRIOR APPLICATION NUMBER: PCT/US01/30661

; PRIOR FILING DATE: 2001-09-28

; PRIOR APPLICATION NUMBER: US 60/245,855

; PRIOR FILING DATE: 2000-11-03

; PRIOR APPLICATION NUMBER: US 60/242,322

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: US 60/240,589

; PRIOR FILING DATE: 2000-10-13

; PRIOR APPLICATION NUMBER: US 60/249,343

; PRIOR FILING DATE: 2000-11-15

; PRIOR APPLICATION NUMBER: US 60/247,587

; PRIOR FILING DATE: 2000-11-09

; PRIOR APPLICATION NUMBER: US 60/245,900

; PRIOR FILING DATE: 2000-11-03

; PRIOR APPLICATION NUMBER: US 60/242,223

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: US 60/236,546

; PRIOR FILING DATE: 2000-09-29

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PERL Program

; SEQ ID NO 4

; LENGTH: 797

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No: 644692CD1

; US-11-241-956-4

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
FILE REFERENCES: 39870-33303RIC300C1
CURRENT APPLICATION NUMBER: US/10/973,115B
CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 10/145,747
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: US 10/028,072
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/581,742
PRIOR FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: PCT/US00/05746
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/135,736
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 60/123,090
PRIOR FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 406
LENGTH: 693
TYPE: PRT
ORGANISM: Homo sapiens
US-10-973-115B-406

Query Match 7.6%; Score 182; DB 6; Length 693;
Best Local Similarity 22.6%; Pred. No. 6.4e-09;
Matches 83; Conservative 46; Mismatches 122; Indels 116; Gaps 14;

QY 91 GSWAARNVSECQELNNEKKS-----KVYHVAVIINYLGHCHS 130
DB 359 GHSS-----AGCTVRRRETQTCFNCNLTYPFAVLWSSVEVDVHKHYLSLLSVGCVWS 414
QY 131 LVALLVAVLFLRLPGCTHGWGDGALVGPWAGPQVRSIRCLNIIHNNLISA 190
DB 415 ALACLVTIAAYL-----C-----SRVPLPCRKRPRDYTIKVMNLLLA 452
QY 191 FILRNATWVQVLTMSPEVHQSNGVRCVLTAAAYNPHVNTNFWMFGECCYLHTAIVL-- 248
DB 453 VFLLDTSP-----LLSEPVALTGSENGCRASAIPLHFSLLTCLSNWGLEGNLRLVVEVF 508
QY 249 -TVSTDLRLKRMFCIGWGPPIIIVAWAIGKLYDNEKCFKRGKPGVYTDYIYQGMIL 307
DB 509 GTVPGYLLK--LSAMGWG--FPIFLVTLVALVDVN-----YGBIIL 547
QY 308 VL-----LINFIFLN-----IVRILMTKLRASTTS 333
DB 548 AVHRTPEGVIYPSMCWIRDSLSVYITNLGLFLVFLFNMAMLATMVVQIIL--RLRPH-- 603
QY 334 ETIQYKAVKATLVLLPLLGITTYMLFPVNPGEDEVSRVVFYFNFSFQGFVSVFYC 393
DB 604 ---QKSHVLTLLGLSLVILGLPALIFPSPASGTGFLV--LYLFSIITSFQGLFIPIWY 659
QY 394 FLNSEVR 400
DB 660 SMELQAR 666

RESULT 13
US-11-241-956-7
Sequence 7, Application US/11241956
Publication No. US20060024792A1
GENERAL INFORMATION:
APPLICANT: INCITE GENOMICS INC.; BAUGHN, Mariah R.;
APPLICANT: GAUL Richard C.; CHAWLA, Narinder K.;
APPLICANT: GANDHI, Ameena R.; HAFALIA, April J.A.;
APPLICANT: RAMKUMAR, Javalakxmi; TRIBOULEY, Catherine M.;
APPLICANT: THORNTON, Michael B.; KALLICK, Deborah A.;
APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;
APPLICANT: BURFORD, Neil; KHAN, Farrah A.;
APPLICANT: YUS, Henry; LU, Yan;

APPLICANT: ARVIZU, Chandra S.; ROOPA, Reddy M.;
APPLICANT: NGUYEN, Danniell B.; LEE, Ernestine A.;
APPLICANT: LU, Dying Aina M.; ISON, Craig H.;
APPLICANT: WALSH, Roderick T.; POLICKY, Jennifer L.
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0236 USN
CURRENT APPLICATION NUMBER: US/11/241,956
CURRENT FILING DATE: 2005-10-04
PRIOR APPLICATION NUMBER: US/10/398,036
PRIOR FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30661
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 60/245,855
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/242,322
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/240,589
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/249,343
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 60/247,587
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/245,900
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/242,223
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/236,546
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PERL Program
SEQ ID NO 7
LENGTH: 549
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 55012817CD1
US-11-241-956-7

Query Match 7.0%; Score 166; DB 7; Length 549;
Best Local Similarity 23.8%; Pred. No. 1.5e-07;
Matches 72; Conservative 43; Mismatches 120; Indels 68; Gaps 12;

QY 117 HVAIVNYIGCHTSLVALLVAVLFLRLRPGCTHGWGDGALVGPWAGPQVRSI 176
DB 266 HILTRISQAGCGVSMIFLAFTIILYAFRLSLRFRKSE-----DAP----- 306
QY 177 RCLNIIHNNLISAFILRNATWVQVLTMSPEVHQSNGV-----KCLVTAAYNY 226
DB 307 -----KIHVALGSLFLNLALFLV-----NVSGSKGSDAACWAR--GAVFHY 347
QY 227 FHVTFNFWMFGECCYLHTAIVLTYSTDLRLKMMFI-CIGMGVFPPIIVAWAIGLY---- 281
DB 348 FLTCATWNGLEAFHLYLLAVRVNTYFHYFLKLSLVGWLPAWLVIGTGSANSYGLYT 407
QY 282 ---YDN-----EKWFGKRGVYTDYI-YQGMILVLLINIFILFNIVRILMTKLRASTTS 333
DB 408 IRDRNRTSLCLCWFPREGTTMVALYITVHGYYFLITFLFGHVVLLAVVWKIFTLRATAVK 467
QY 334 ETIQYKAVKATLVLLPLLGITTYMLFPVNP-GEDEVSRVVFYFNFSFQGFVSVFY 392
DB 468 ERGNKRVKLVLLGLSLVGLVGTWGLAIFTPLGLSTV--YIFALFN-----SLQGVFICWF 521
QY 393 CFL 395
DB 522 TIL 524

RESULT 14
US-11-200-822-3
Sequence 3, Application US/11200822
Publication No. US20060040302A1
GENERAL INFORMATION:
APPLICANT: INCITE GENOMICS INC.; BAUGHN, Mariah R.;
APPLICANT: GAUL Richard C.; CHAWLA, Narinder K.;
APPLICANT: GANDHI, Ameena R.; HAFALIA, April J.A.;
APPLICANT: RAMKUMAR, Javalakxmi; TRIBOULEY, Catherine M.;
APPLICANT: THORNTON, Michael B.; KALLICK, Deborah A.;
APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;
APPLICANT: BURFORD, Neil; KHAN, Farrah A.;
APPLICANT: YUS, Henry; LU, Yan;

```
; APPLICANT: Bostein, et al.
; TITLE OF INVENTION: Methods of Classifying, Diagnosing, Stratifying and
; FILE REFERENCE: 2002850-0049
; CURRENT APPLICATION NUMBER: US/11/200,822
; CURRENT FILING DATE: 2005-08-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2923
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cadherin EGF
; OTHER INFORMATION: LAG Seven Pass G-Type Receptor 2
US-11-200-822-3

Query Match      6.9%; Score 165; DB 7; Length 2923;
Best Local Similarity 22.3%; Pred. No. 1.3e-06;
Matches 78; Conservative 64; Mismatches 113; Indels 94; Gaps 19;

QY 91 GSWAARVNVSECOELL-NEEKSKVHVHV---AVI-----INVLGHCHIS 130
Db 2332 GGWSAR----GCSVVRNESHVSCQCNHMTSFAYLMDVSRNGEILPLKLTLYVALGVT 2387

QY 131 LVALLVAFVFLRLRPGCTHMGDQADGAEVGPAGWSGAPPQVRRSIRCLRNIIHWNLISA 190
Db 2388 LAALLTLP-FFLT-----LRLSRNHG----- 2410

QY 191 FILRN--ATWFFVQVLTSPRVHNSGVN-CRLVTAAYNYFHVNFPMFGGCVLHTAI- 246
Db 2411 -IRNLTAALGLAQLVFLGQINQADLPFACTVAILLHFLYCTFSWALLEALHLYRALT 2469

QY 247 -VLTYSIDRLRKWMPICIGVGPPIIVAWAIG---KLYVDNEKCHFGKRPVYTDYI-- 300
Db 2470 EVRDVTGPMR--FYMLGHWGP-AFITGLAQLDPGEGYNPDFCWL-----SIYDTLWS 2522

QY 301 YQCGPMILVLLINFIPLNIVRILMTKLRASTTGETIQYRK-----AVKATLVLLPLGIT 355
Db 2523 FAGVAFVAVSM8-VFLY-----ILAAASCAQRQGFKKGVSGLOPSFAVLLLSAT 2575

QY 356 YMLFFVNPGBDESVRVVFIYFNSFLBSFQGFVSVFYCFNLSNVSRAIR 404
Db 2576 WLLALLSVNSD---TLLFHYLFATCNCIQGPFIFLSYVLSKVEVRKALK 2621

RESULT 15
US-11-241-956-2
; Sequence 2, Application US/11241956
; Publication No. US20060024792A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS INC.; BAUGHN, Mariah R.;
; APPLICANT: GAUL Richard C.; CHAWLA, Narinder K.;
; APPLICANT: GANDHI, Ameena R.; HAFALIA, April J.A.;
; APPLICANT: RAMKUMAR, Jayalaxmi; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael B.; KALLICK, Deborah A.;
; APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;
; APPLICANT: BURFORD, Neil; KHAN, Farrah A.;
; APPLICANT: YUE, Henry; LU, Yan;
; APPLICANT: ARVIZU, Chandra S.; ROOPA, Reddy M.;
; APPLICANT: NGUYEN, Dannel B.; LEE, Ernestine A.;
; APPLICANT: LU, Dyung Aina M.; ISON, Craig H.;
; APPLICANT: WALSH, Roderick T.; POLICKY, Jennifer L.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: FI-0236 USN
; CURRENT APPLICATION NUMBER: US/11/241,956
; CURRENT FILING DATE: 2005-10-04
; PRIOR APPLICATION NUMBER: US/10/398,036
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: PCT/US01/30661
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/245,855
; PRIOR FILING DATE: 2000-11-03
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; PRIOR APPLICATION NUMBER: US 60/242,322
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/240,589
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/249,343
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/247,587
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/245,900
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/242,223
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/236,546
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 578
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7477708CD1
US-11-241-956-2

Query Match      6.8%; Score 163; DB 7; Length 578;
Best Local Similarity 25.2%; Pred. No. 3e-07;
Matches 71; Conservative 51; Mismatches 108; Indels 52; Gaps 16;

QY 118 VAVIINYLGHCHISLVALVFLRLRPGCTHMGDQADGAEVGPAGWSGAPPQVRRS-I 176
Db 315 ILTYITVVGIGISLSLILCL-----SIEV-LVMS---QVTKTEI 350

QY 177 RCLRNIIHWNLISAFILRNATWFFVQVLTWS-PRVHQSNGVGCRLVTAAYNYFHVNFPM 235
Db 351 TYLRHVCIYN-IAATLMDVWVFIVASFLSGPITHKG---CVAATFFVHFVFLSVFFPM 406

QY 236 FGGCVLHTAIVLTVSTDRLRKWMFIC---IGWGVPPPI---IVAWAIGKLYYDNEKC 287
Db 407 LAKALLILYIMIVFHT--LPKSVLVASLPSVGYGCLAIATAITVAATPEGKGYLPEIC 464

QY 288 WFG-KRPGVYTDYIYQGPMLVLLINFIPLNIVRILMTKLRASTTSETIQYRKAV---- 342
Db 465 WLNWDMTKALLAFVI--PALAIWVN---LITVTLVIVKTQRAAIGNSMFMQEVRAIVRIS 519

QY 343 KATLVLLPLILGITYMLFPVNPGEDEVSRVVFYFNSFLESFQ 384
Db 520 KNTAILTPLLGLTWG-FGVATVIDDRSLAFPHIF-SLLNAFQ 559
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Search completed: March 16, 2006, 17:25:15

Job time : 23 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match					
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2	1582	100.0	1582	8	ABX93041	Abx93041 Human cor	
3	1582	100.0	1582	9	ABX11840	Abx11840 Human cDN	
4	1582	100.0	1582	12	ADJ65809	Adj65809 Human cor	
5	1398	88.4	1495	2	AAQ81952	AAq81952 Human plt	
6	1398	88.4	1495	2	AAT28968	Aat28968 Human CRF	
7	1398	88.4	1495	6	AD44482	Aad44482 Human CRF	
8	1398	88.4	1495	8	ABX93034	Abx93034 Human cor	
9	1398	88.4	1495	9	ABX11833	Abx11833 Human cDN	
10	1398	88.4	1495	12	ADJ65796	Adj65796 Human cor	
11	1398	88.4	2579	6	AA62243	AA62243 cDNA sequ	
12	1396.4	88.3	2536	12	ADO23851	Ado23851 Human GPC	
13	1396.4	88.3	2536	12	ADO50782	Ado50782 Human cor	
14	1335	84.4	1335	10	ACA56762	ACA56762 Human eig	
15	1335	84.4	1335	12	ADI56558	ADI56558 Human pol	
16	1188	75.1	1285	6	AAU49972	Aal49972 Human cor	
17	1188	75.1	1285	12	ADO50784	Ado50784 Human cor	
18	1167.4	73.8	1278	2	ABT37068	Abt37068 Human cor	
19	1157.2	73.0	10042	6	AKK95585	Abk95585 Yeast rep	

Human; gene; ss; corticotropin-releasing factor receptor; CRF;
 G protein-coupled corticotropin-releasing factor receptor;
 hypothalamic peptide; pituitary adrenocorticotrophic hormone; ACTH;
 adrenal glucocorticoid; gene therapy; cortisol; Alzheimer's disease;
 Cushing's disease; anorexia nervosa; alcoholism; antiinflammatory;
 irritable bowel syndrome; melancholic depression; neuroprotective;
 nootropic; antidepressant; splice variant.
 Homo sapiens.

Key Location/Qualifiers
 CDS 82..1416
 /*tag= a
 /product= "CRF-R2"

US6495343-B1.
 17-DEC-2002.
 17-JAN-1995; 95US-00374009.
 18-JUN-1993; 93US-00079320.
 23-AUG-1993; 93US-00110286.
 25-MAY-1994; 94MO-US005908.
 09-DEC-1994; 94US-00353537.
 (SALK) SALK INST BIOLOGICAL STUDIES.
 Perrin MH, Chen R, Lewis KA, Vale MW, Donaldson CJ, Sawchenko P;
 WPI; 2003-327461/31.
 P-PSDB; ABU08081.

New nucleic acid and its encoded G protein-coupled corticotropin-releasing factor receptor, useful for diagnosing or treating e.g. ACTH levels or high cortisol levels associated with Alzheimer's disease or Cushing's disease.
 Disclosure; Col 57-62; 42pp; English.

The invention discloses an isolated nucleic acid, which encodes a mammalian G protein-coupled corticotropin-releasing factor (CRF) receptor protein. CRF is a hypothalamic peptide which stimulates the secretion and biosynthesis of pituitary adrenocorticotrophic hormone (ACTH) leading to increased adrenal glucocorticoid production. The nucleic acid, or the CRF receptor that it encodes, is useful in bioassays. The nucleic acid or CRF receptor is particularly useful for providing recombinant receptors that allows the development of less expensive, more sensitive and automated means for assaying CRF and CRF-like compounds and developing CRF-based therapeutics. The nucleic acid, or fragments of its encoded receptor, are useful in therapy, e.g. gene therapy for reducing ACTH levels or treating high cortisol levels associated with Alzheimer's disease, Cushing's disease, anorexia nervosa, alcoholism or irritable bowel syndrome. These are also useful in diagnostic assays, e.g. for diagnosing Alzheimer's disease, melancholic depression, anorexia nervosa, Cushing's disease or alcoholism. The sequence presented is the human splice variant of CRF-R1, CRF-R2, CDNA

Sequence 1582 BP; 286 A; 518 C; 437 G; 341 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1582; DB 8; Length 1582;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAGCCGCGAGCCGCGCGGTCCTCTGGGATGTCGGTAGGACCCGGGCATTGAGGAC 60
 DB 1 CGAGCCGCGAGCCGCGCGGTCCTCTGGGATGTCGGTAGGACCCGGGCATTGAGGAC 60
 QY 61 GGATGCGGAGCCGAGCGGATGGGAGGACCCCGCAGCTCCGCTCTCGTCAAGGCCCTT 120
 DB 61 GGATGCGGAGCCGAGCGGATGGGAGGAGCCCGCAGCTCCGCTCTCGTCAAGGCCCTT 120
 QY 121 CTCCTTCTGGGGGTGAACCCCGTCTCTGCTCCCTCCAGGACCGACACTCGGAGCGCTG 180

121 CTCCTTCTGGGGGTGAACCCCGTCTCTGCTCCCTCCAGGACCGACACTCGGAGAGCTG 180
 QY 181 TCCTTGGCCGAGCAACATCTCAGGACTGCAGTCAAGCGCATCCGTGGACCTCATTTGGCACC 240
 DB 181 TCCTTGGCCGAGCAACATCTCAGGACTGCAGTCAAGCGCATCCGTGGACCTCATTTGGCACC 240
 QY 241 TGTGCGCCGCGAGCCCTGCGGGGAGCTAGTGGTTCGGCCCTGCGCTGCTTTTCTAT 300
 DB 241 TGTGCGCCGCGAGCCCTGCGGGGAGCTAGTGGTTCGGCCCTGCGCTGCTTTTCTAT 300
 QY 301 GGTGTCGGCTACAAATACCAACAATGGCTACCGGAGTGCCTGGCCAAATGGCAGCTGG 360
 DB 301 GGTGTCGGCTACAAATACCAACAATGGCTACCGGAGTGCCTGGCCAAATGGCAGCTGG 360
 QY 361 GCCGCCCGGTGAATTAATTCAGAGTCCAGGAGATCCTCAATGAGGAGAAAAAGCAAG 420
 DB 361 GCCGCCCGGTGAATTAATTCAGAGTCCAGGAGATCCTCAATGAGGAGAAAAAGCAAG 420
 QY 421 GTGCACTACATGTCGAGTCACTCACTCTGGGCCACTGTATCTCCCTGGTGGCC 480
 DB 421 GTGCACTACATGTCGAGTCACTCACTCTGGGCCACTGTATCTCCCTGGTGGCC 480
 QY 481 CTCCTGCTGGCTTTCT 540
 DB 481 CTCCTGCTGGCTTTCT 540
 QY 541 CAGGAGATGAGCCCTCTGGAGTGGGGGCTCCATGAGTGGTGGCCCATTTACAGTTTCTGA 600
 DB 541 CAGGAGATGAGCCCTCTGGAGTGGGGGCTCCATGAGTGGTGGCCCATTTACAGTTTCTGA 600
 QY 601 AGGAGATCCGGTCTCGAATCACTCACTGGAACTCATCTCTCGCTGCTCATCTG 660
 DB 601 AGGAGATCCGGTCTCGAATCACTCACTGGAACTCATCTCTCGCTGCTCATCTG 660
 QY 661 CGCAAGCCCACTGGTTCGAGTAACTAGAGCCCGAGGTCCACGAGGAGCAAC 720
 DB 661 CGCAAGCCCACTGGTTCGAGTAACTAGAGCCCGAGGTCCACGAGGAGCAAC 720
 QY 721 GTGGGCTGGTGCAGGTTGGTGACAGCGGCTCACTTCCATGTGACCAACTTCTTTC 780
 DB 721 GTGGGCTGGTGCAGGTTGGTGACAGCGGCTCACTTCCATGTGACCAACTTCTTTC 780
 QY 781 TGAATGTTGGCGAGGGTGTACTGTCACAGCACTGCTGTCTACTCTCACTGAC 840
 DB 781 TGAATGTTGGCGAGGGTGTACTGTCACAGCACTGCTGTCTACTCTCACTGAC 840
 QY 841 CGGCTGGCAATGGATGTTTCATCTGCTGGTGGGTGGTGGCTTCCCATCATTTGTG 900
 DB 841 CGGCTGGCAATGGATGTTTCATCTGCTGGTGGGTGGTGGCTTCCCATCATTTGTG 900
 QY 901 GCCTGGGCCATTGGGAAGCTGTACTACGCAATGAGAGTGTGGTTGGCAAAAGGCTT 960
 DB 901 GCCTGGGCCATTGGGAAGCTGTACTACGCAATGAGAGTGTGGTTGGCAAAAGGCTT 960
 QY 961 GGGGTGTACACCGACTACATCTACAGGGGCCCATGATCTGCTGCTGATCAATTC 1020
 DB 961 GGGGTGTACACCGACTACATCTACAGGGGCCCATGATCTGCTGCTGATCAATTC 1020
 QY 1021 ATCTTCTTTTCAACATGTCCTCCATCTCATGACCAAGTCCGGGATCCACCACTCT 1080
 DB 1021 ATCTTCTTTTCAACATGTCCTCCATCTCATGACCAAGTCCGGGATCCACCACTCT 1080
 QY 1081 GAGACCAATTGAGTACAGGAGGCTGTGAAAGCCACTCTGCTGCTGCTGCTGCTGCTGCTG 1140
 DB 1081 GAGACCAATTGAGTACAGGAGGCTGTGAAAGCCACTCTGCTGCTGCTGCTGCTGCTGCTG 1140
 QY 1141 ATCACCTACATGCTGTTCTTCTGTCATCCCGGGGAGGATGAGGTCTCCCGGGTCTTTC 1200
 DB 1141 ATCACCTACATGCTGTTCTTCTGTCATCCCGGGGAGGATGAGGTCTCCCGGGTCTTTC 1200
 QY 1201 ATCTACTTCACT 1260

QY 481 CTCCTGGTGGCCCTTTGTCCTCTTTCTGGGCTCAGGCCAGGCTGCACCCATTTGGGGTGAC 540
Db 481 CTCCTGGTGGCCCTTTGTCCTCTTTCTGGGCTCAGGCCAGGCTGCACCCATTTGGGGTGAC 540
QY 541 CAGGCAGATGGAGCCCTTGAGGTGGGGCTCCATGGAGTGGTCCCCCATTTCAAGGTTGGA 600
Db 541 CAGGCAGATGGAGCCCTTGAGGTGGGGCTCCATGGAGTGGTCCCCCATTTCAAGGTTGGA 600
QY 601 AGGAGCATCCGGTGCCTCGAATCATCATCCACTGGAACTCATCTCCGCTTTCCTG 660
Db 601 AGGAGCATCCGGTGCCTCGAATCATCATCCACTGGAACTCATCTCCGCTTTCCTG 660
QY 661 CGCAAGCCACCTGGTGTGGTCCAGTAAACATGAGGCCCGAGTCCACAGAGCAAC 720
Db 661 CGCAAGCCACCTGGTGTGGTCCAGTAAACATGAGGCCCGAGTCCACAGAGCAAC 720
QY 721 GTGGGCTGGTGAGGTGGTGACAGCGCTCAACACTTCTTCCATGAGCAACTTCTTC 780
Db 721 GTGGGCTGGTGAGGTGGTGACAGCGCTCAACACTTCTTCCATGAGCAACTTCTTC 780
QY 781 TGGATGTTGGCGAGGCTGTCTACCTGCACACAGCCATCGTGTCACTTCACTCCACTGAC 840
Db 781 TGGATGTTGGCGAGGCTGTCTACCTGCACACAGCCATCGTGTCACTTCACTCCACTGAC 840
QY 841 CGGCTGGCAAAATGGATGTTTCATCTGCAATTTGGCTGGGGTGTGCCCTTCCCATCATTTGTG 900
Db 841 CGGCTGGCAAAATGGATGTTTCATCTGCAATTTGGCTGGGGTGTGCCCTTCCCATCATTTGTG 900
QY 901 GCCTGGGCCAATGGGAGCTGTACTACGACAATGAGAAGTGTGGTTTGGCAAAAGGCT 960
Db 901 GCCTGGGCCAATGGGAGCTGTACTACGACAATGAGAAGTGTGGTTTGGCAAAAGGCT 960
QY 961 GGGGTGTACACCGACTACATCTACCGAGGCCCATGATCTCTGTCTGTGATCAATTTTC 1020
Db 961 GGGGTGTACACCGACTACATCTACCGAGGCCCATGATCTCTGTCTGTGATCAATTTTC 1020
QY 1021 ATCTTCTTTTCAACATGTCGCGATCTCTCAAGCAAGCTCCGGGATCCACACAGTCT 1080
Db 1021 ATCTTCTTTTCAACATGTCGCGATCTCTCAAGCAAGCTCCGGGATCCACACAGTCT 1080
QY 1081 GAGACCAATTCAGTACAGGAGGCTGTGAAAGCCACTCTGTGTCTGTCGCCCTCTCTGGG 1140
Db 1081 GAGACCAATTCAGTACAGGAGGCTGTGAAAGCCACTCTGTGTCTGTCGCCCTCTCTGGG 1140
QY 1141 ATCACTTACATGCTGTTCTTTCGTCATCCCGGAGGATGAGGTCTCCCGGTCGTCTTC 1200
Db 1141 ATCACTTACATGCTGTTCTTTCGTCATCCCGGAGGATGAGGTCTCCCGGTCGTCTTC 1200
QY 1201 ATCTACTTCAACTCTTCTTCTGGAATCTTCCAGGGCTTCTTGTGTCTGTCTACTGT 1260
Db 1201 ATCTACTTCAACTCTTCTTCTGGAATCTTCCAGGGCTTCTTGTGTCTGTCTACTGT 1260
QY 1261 TTCTCTCAATAGTGGTCCGTTCTGCCATCCGAGAGGTTGGCACCGTGGCAGGACAAG 1320
Db 1261 TTCTCTCAATAGTGGTCCGTTCTGCCATCCGAGAGGTTGGCACCGTGGCAGGACAAG 1320
QY 1321 CACTTCGATCCGTCGCCAGTGGCCGTCGCATGTCATCCCACTCCCAACCCCGTGC 1380
Db 1321 CACTTCGATCCGTCGCCAGTGGCCGTCGCATGTCATCCCACTCCCAACCCCGTGC 1380
QY 1381 AGCTTTTCAAGCATCAAGCATGTCACAGCATGTCGAGCTGGCAGGTCATGGAGCAGCCCC 1440
Db 1381 AGCTTTTCAAGCATCAAGCATGTCACAGCATGTCGAGCTGGCAGGTCATGGAGCAGCCCC 1440
QY 1441 CAAAGAGCTGTGGTGGGGGATGACGGCAGGCTCCCTGACCACTTGTGTGAGGT 1500
Db 1441 CAAAGAGCTGTGGTGGGGGATGACGGCAGGCTCCCTGACCACTTGTGTGAGGT 1500
QY 1501 GACCTGTTAGTCTCATGTCCTTCCCTCCAGGACGCTGACACTGACAGCTGGGGGG 1560
Db 1501 GACCTGTTAGTCTCATGTCCTTCCCTCCAGGACGCTGACACTGACAGCTGGGGGG 1560

QY 1561 CGCTCTCTCCCTGCGAGCGGTG 1582
Db 1561 CGCTCTCTCCCTGCGAGCGGTG 1582
RESULT 4
ADJ65809
ID ADJ65809 standard; cDNA; 1582 BP.
XX AC ADJ65809;
XX DT 20-MAY-2004 (first entry)
XX DE Human corticotropin-releasing factor receptor CRF-RA2 cDNA.
XX KW Human; corticotropin-releasing factor receptor; CRF-RA2; ss; gene;
KW Alzheimer's disease; melancholic depression; anorexia nervosa;
KW Cushing's disease; hypercortisolemia; alcoholism;
KW gastrointestinal disorder; irritable bowel syndrome; inflammation;
KW Addison's disease; cardiac perfusion; blood pressure; hypotension.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 82..1416
FT /*tag= a
FT /product= "CRF-RA2"
XX PN US2004039173-A1.
XX PD 26-FEB-2004.
XX PF 26-AUG-2003; 2003US-00649193.
XX PR 18-JUN-1993; 93US-00079320.
XX PR 23-AUG-1993; 93US-00110286.
XX PR 25-MAY-1994; 94WO-US005908.
XX PR 09-DEC-1994; 94US-0035537.
XX PR 07-JUN-1995; 95US-0048139.
XX PR 12-NOV-1998; 98US-00191724.
XX (SALK) SALK INST BIOLOGICAL STUDIES.
XX PI Perrin MH, Chen R, Lewis KA, Vale WW, Donaldson CJ, Sawchenko P;
XX WPI; 2004-203293/19.
XX P-PSDB; ADJ65810.
XX PT New mammalian G protein-coupled corticotropin-releasing factor receptor
XX protein, useful in diagnosing and treating Alzheimer's disease, anorexia
XX nervosa, Cushing's disease, alcoholism, irritable bowel syndrome or
XX hypotension.
XX PS Claim 1; SEQ ID NO 14; 44pp; English.
XX CC The invention relates to an isolated mammalian G protein-coupled
XX corticotropin-releasing factor (CRF) receptor protein or polypeptide from
XX Rat, Mouse or human appearing as ADJ65801, ADJ65803, ADJ65805, or
XX ADJ65810, encoded by the nucleic acids appearing as ADJ65800, ADJ65802,
XX ADJ65804, or ADJ65809. Also included are a composition comprising CRF-R,
XX an antibody generated against CRF-R and a diagnostic kit, for assaying
XX for the presence in biological fluids of CRF-R protein, protein analogues
XX and/or fragments, comprising CRF-R) and/or one or more antibodies. The
XX protein, polynucleotide or composition is useful in diagnosing and
XX treating Alzheimer's disease, melancholic depression, anorexia nervosa,
XX Cushing's disease, hypercortisolemia or alcoholism, gastrointestinal
XX disorders (e.g. irritable bowel syndrome) or physiological conditions
XX (e.g. inflammation or Addison's disease), in regulating cardiac perfusion
XX and in modulating blood pressure, thus combat hypotension. The present
XX sequence encodes human splice variant CRF-RA2.
SQ Sequence 1582 BP; 286 A; 518 C; 437 G; 341 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1582;	DB 12;	Length 1582;
Best Local Similarity	100.0%;	Prod. No. 0;		
Matches 1582;	Conservative	0;	Mismatches	0;
	Indels	0;	Gaps	0;
Qy	1	CGAGCCCGACGCGCCCGCTTCCTCTGGGATGTCCGTAGGACCCCGGCATTCAGGAC	60	
Db	1	CGAGCCCGACGCGCCCGCTTCCTCTGGGATGTCCGTAGGACCCCGGCATTCAGGAC	60	
Qy	61	GGTAGCCGAGCGAGCCCGAGGATGGAGGGCAACCGCAGCTCCGTCTCGTCAAGGCCCTT	120	
Db	61	GGTAGCCGAGCGAGCCCGAGGATGGAGGGCAACCGCAGCTCCGTCTCGTCAAGGCCCTT	120	
Qy	121	CTCCTTTGGGGCTGAACCCCGTCTCTGCTCCCTCCAGACAGACACTGCGAGAGCTG	180	
Db	121	CTCCTTTGGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACACAGCACTGCGAGAGCTG	180	
Qy	181	TCCCTGGCCAGCAACATCTCAGGACTCGAGTGCAACGCATCCGTGGACCTCATTTGGCACC	240	
Db	181	TCCCTGGCCAGCAACATCTCAGGACTCGAGTGCAACGCATCCGTGGACCTCATTTGGCACC	240	
Qy	241	TGCTGGGCCCGCAGCCCTTGCGGGCGAGCTAGTGGTTTGGGCCCTGCCTCTTTTCTAT	300	
Db	241	TGCTGGGCCCGCAGCCCTTGCGGGCGAGCTAGTGGTTTGGGCCCTGCCTCTTTTCTAT	300	
Qy	301	GGTGTCCGCTACAATAACACAAAACAATGGCTACCGGAGTGCCCTGGGCAATGGCAGCTGG	360	
Db	301	GGTGTCCGCTACAATAACACAAAACAATGGCTACCGGAGTGCCCTGGGCAATGGCAGCTGG	360	
Qy	361	GCGCCCGCGTAATTAATCTCGAGTGGCCAGAGATCTCTCAATGAGGAGAAAAAGCAAG	420	
Db	361	GCGCCCGCGTAATTAATCTCGAGTGGCCAGAGATCTCTCAATGAGGAGAAAAAGCAAG	420	
Qy	421	GTGCACCTACCATGTGCGAGTCAATCAACTGCGGCCACTGTATCTCCCTGGTGCC	480	
Db	421	GTGCACCTACCATGTGCGAGTCAATCAACTGCGGCCACTGTATCTCCCTGGTGCC	480	
Qy	481	CTCTGTGGCTTTGTGCTCTTTCTGCGCTCAGGCCAGGCTGCACCCATTTGGGGTGAC	540	
Db	481	CTCTGTGGCTTTGTGCTCTTTCTGCGCTCAGGCCAGGCTGCACCCATTTGGGGTGAC	540	
Qy	541	CAGCAGATGAGAGCCCTGGAGGTGGGGCTCCATGGAGTGGTGCCCATTTCAGGTTGCA	600	
Db	541	CAGCAGATGAGAGCCCTGGAGGTGGGGCTCCATGGAGTGGTGCCCATTTCAGGTTGCA	600	
Qy	601	AGGAGCATCCGGTGCCTCGCAAAACATCAATCCACTGGAAACCTCATCTCGGCTTCATCTG	660	
Db	601	AGGAGCATCCGGTGCCTCGCAAAACATCAATCCACTGGAAACCTCATCTCGGCTTCATCTG	660	
Qy	661	CGCAACGCCACCTGGTTCCAGTCCAGTAAACCATGAGCCCGGAGGTCACACAGCAAC	720	
Db	661	CGCAACGCCACCTGGTTCCAGTCCAGTAAACCATGAGCCCGGAGGTCACACAGCAAC	720	
Qy	721	GTGGGCTGGTGACAGTTGGTGACAGCGCCTACAACCTACTTCCATGTGACCACTTCTTC	780	
Db	721	GTGGGCTGGTGACAGTTGGTGACAGCGCCTACAACCTACTTCCATGTGACCACTTCTTC	780	
Qy	781	TGGATGTTTGGCGAGGGCTGCTACTGTCACACAGCCATCGTGCTCACTCTCCACTGAC	840	
Db	781	TGGATGTTTGGCGAGGGCTGCTACTGTCACACAGCCATCGTGCTCACTCTCCACTGAC	840	
Qy	841	CGGCTGGCCAAATGGATGTTTCATCTGCATTTGGCTGGGGTGTGCCCTTCCCATCATTTGTG	900	
Db	841	CGGCTGGCCAAATGGATGTTTCATCTGCATTTGGCTGGGGTGTGCCCTTCCCATCATTTGTG	900	
Qy	901	GCCTGGGCCAATGGGAAGCTGTACTACGAACAATGAGAAGTGCTGGTTGGCAAAAGGCTT	960	
Db	901	GCCTGGGCCAATGGGAAGCTGTACTACGAACAATGAGAAGTGCTGGTTGGCAAAAGGCTT	960	
Qy	961	GGGGTGTACACCGACTACATCTACAGGGCCCATGATCTCTGGTCTCTGCTGATCAATTTTC	1020	
Db	961	GGGGTGTACACCGACTACATCTACAGGGCCCATGATCTCTGGTCTCTGCTGATCAATTTTC	1020	
Qy	1021	ATCTTCTCTTTTCAACATCGTCCGATCCTCATGTGACCAAGCTCCGGGATCCACCACTCT	1080	

[illegible]

XX WPI: 1995-052077/07.
DR P-PSDB; AAR69519.
XX
PT Isolated corticotropin releasing factor receptor and nucleic acid - also
PT antibodies, useful for diagnosis and treatment of Cushing's disease,
PT pituitary tumours etc., also to identify specific agonists and
PT antagonists.
XX
PS Claim 6; Page 63; 84pp; English.
XX
CC The protein encoded by this sequence can be used to determine CRF (e.g.
CC over- or under-production, high levels of CRF late in pregnancy may
CC indicate risk of premature labor). Cells expressing the protein are used
CC to identify e.g. antibodies, which can be used to modulate signal
CC transduction activity mediated by CRF receptors. Typical applications are
CC in the treatment of Cushing's disease, pituitary tumors, etc. (Updated on
CC 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 1495 BP; 271 A; 496 C; 403 G; 325 T; 0 U; 0 Other;

Query Match 88.4%; Score 1398; DB 2; Length 1495;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 1 CGAGCCCGAGCCGCGCCGCTTCTCTGGGATGTCCTGAGACCCGGGCAATTCAGGAC 60
DB 1 CGAGCCCGAGCCGCGCCGCTTCTCTGGGATGTCCTGAGACCCGGGCAATTCAGGAC 60

QY 61 GGTAGCCGAGCGAGCCGAGGATGGAGGACCCCGCAGCTCCGTCTCGTCAAGGCCCTT 120
DB 61 GGTAGCCGAGCGAGCCGAGGATGGAGGACCCCGCAGCTCCGTCTCGTCAAGGCCCTT 120

QY 121 CTCCTCTCGGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCACTGCGAGAGCCTG 180
DB 121 CTCCTCTCGGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCACTGCGAGAGCCTG 180

QY 181 TCCTGCGCCAGCAACATCTCAGGACTGAGTGCAGCAATCGGTGCGACCTCATTTGGCACC 240
DB 181 TCCTGCGCCAGCAACATCTCAGGACTGAGTGCAGCAATCGGTGCGACCTCATTTGGCACC 240

QY 241 TGCTGGCCCGCAGCCCTCGGGGACGCTAGTGGTTCGGCCCTCGCCCTGCTTTTCTAT 300
DB 241 TGCTGGCCCGCAGCCCTCGGGGACGCTAGTGGTTCGGCCCTCGCCCTGCTTTTCTAT 300

QY 301 GGTGTCGCTACAAATACCAAAACAATGGCTACCGGGAGTGCCTGGGCAATGGCAGCTGG 360
DB 301 GGTGTCGCTACAAATACCAAAACAATGGCTACCGGGAGTGCCTGGGCAATGGCAGCTGG 360

QY 361 GCGCCCGCGTGAATTAATCCGAGTGCAGAGATCTCAATGAGGAGAAAAAAGCAAG 420
DB 361 GCGCCCGCGTGAATTAATCCGAGTGCAGAGATCTCAATGAGGAGAAAAAAGCAAG 420

QY 421 GTGCACCTACCAATGTCGAGTCAATCACTACCTGGGCCACTGTATCTCCCTGGTGCC 480
DB 421 GTGCACCTACCAATGTCGAGTCAATCACTACCTGGGCCACTGTATCTCCCTGGTGCC 480

QY 481 CTCTGGTGGCTTTGCTCTTCTGCGGCTCAGGCGCAGGCTGCACCCATTTGGGGTGAC 540
DB 481 CTCTGGTGGCTTTGCTCTTCTGCGGCTCAGGCGCAGGCTGCACCCATTTGGGGTGAC 540

QY 541 CAGGACAGTGGAGCCCTGGAGGTGGGGGCTCCATGGAGTGGTGGCCCATTTTCAGTTTGA 600
DB 541 ----- 513

QY 601 AGGAGCATCCGCTGCGGAAACATATCCACTGGAACTCATCTCGGCTTCATCTG 660
DB 514 AGGAGCATCCGCTGCGGAAACATATCCACTGGAACTCATCTCGGCTTCATCTG 573

QY 661 CGCAACGCCACCTGGTTCTGTTCCAGTCAACATGAGCCCGGAGGTCACAGAGCAAC 720
DB 574 CGCAACGCCACCTGGTTCTGTTCCAGTCAACATGAGCCCGGAGGTCACAGAGCAAC 633

QY 721 GTGGGCTGGTGAGGTTGGTGACAGCGCGCTACAACTACTTCCATGTGACCAACTTCTTC 780
DB 634 GTGGGCTGGTGAGGTTGGTGACAGCGCGCTACAACTACTTCCATGTGACCAACTTCTTC 693

QY 781 TGGATGTTGGCGAGGGCTCTACTACCTGCGACACAGCCATCGTGTCACTACTCCACTGAC 840
DB 694 TGGATGTTGGCGAGGGCTCTACTACCTGCGACACAGCCATCGTGTCACTACTCCACTGAC 753

QY 841 CGGCTGGCAAAATGGATGTTTCATCTGCAATTTGGGTGGGGTGTGCCCTTCCCATCATTTGTG 900
DB 754 CGGCTGGCAAAATGGATGTTTCATCTGCAATTTGGGTGGGGTGTGCCCTTCCCATCATTTGTG 813

QY 901 GCCTGGGCCAATTCGGAGGCTGTACTACGACAATGAGAAGTGTGGTTTGCAGAAAGCCCT 960
DB 814 GCCTGGGCCAATTCGGAGGCTGTACTACGACAATGAGAAGTGTGGTTTGCAGAAAGCCCT 873

QY 961 GGGGTGTACACCGACTACATCTACCGAGGCGCCCATGATCTCTGTCTGTGATCAATTC 1020
DB 874 GGGGTGTACACCGACTACATCTACCGAGGCGCCCATGATCTCTGTCTGTGATCAATTC 933

QY 1021 ATCTTCTTTTCAACATCGTCCGGATCTCATGACCAAGCTCCGGGATCCACCACTCT 1080
DB 934 ATCTTCTTTTCAACATCGTCCGGATCTCATGACCAAGCTCCGGGATCCACCACTCT 993

QY 1081 GAGACCAATTCAGTACAGGAGGCTGTGAAGCCACTCTGTGTGTCTGCTGCCCTCTCTGGC 1140
DB 994 GAGACCAATTCAGTACAGGAGGCTGTGAAGCCACTCTGTGTGTCTGCTGCCCTCTCTGGC 1053

QY 1141 ATCACTTACATGCTGTTCTTCTGTCATCCCGGGAGGATGAGGTCTCCCGGCTCGTCTTC 1200
DB 1054 ATCACTTACATGCTGTTCTTCTGTCATCCCGGGAGGATGAGGTCTCCCGGCTCGTCTTC 1113

QY 1201 ATCTACTTCAACTCTTCTGGAATCTTCCAGGGCTTCTTTGTGTGTCTGTCTACTGT 1260
DB 1114 ATCTACTTCAACTCTTCTGGAATCTTCCAGGGCTTCTTTGTGTGTCTGTCTACTGT 1173

QY 1261 TTCTCAATAGTACGCTCCGTTCTGCGATCCGGAAGAGGTGGCACCGGTGGCAGGACAAG 1320
DB 1174 TTCTCAATAGTACGCTCCGTTCTGCGATCCGGAAGAGGTGGCACCGGTGGCAGGACAAG 1233

QY 1321 CACTCGATCCGTCGCGAGTGGCCCGTGCATGTCCATCCCGACCTCCCGCAACCCGCTGTC 1380
DB 1234 CACTCGATCCGTCGCGAGTGGCCCGTGCATGTCCATCCCGACCTCCCGCAACCCGCTGTC 1293

QY 1381 AGTTTTCACAGCATCAAGCAGTCCACAGAGTCTGAGCTGGCAGGTCAATGGAGCAGCCCC 1440
DB 1294 AGTTTTCACAGCATCAAGCAGTCCACAGAGTCTGAGCTGGCAGGTCAATGGAGCAGCCCC 1353

QY 1441 CAAAGAGCTGTGGTGGGGGATGACGGCCAGGCTCCCTGACCACTGCTGTGGAGGT 1500
DB 1354 CAAAGAGCTGTGGTGGGGGATGACGGCCAGGCTCCCTGACCACTGCTGTGGAGGT 1413

QY 1501 GACTGTGTAGTCTCATGCCACTTCCCGCAGGAGCAGTGGCACTGACAGCTGGGGGGG 1560
DB 1414 GACTGTGTAGTCTCATGCCACTTCCCGCAGGAGCAGTGGCACTGACAGCTGGGGGGG 1473

QY 1561 CCGCTCTCCCGCTGCGAGCCGTTG 1582
DB 1474 CCGCTCTCCCGCTGCGAGCCGTTG 1495

RESULT 6

AAT28968

ID AAT28968 standard; cDNA; 1495 BP.

XX

AC AAT28968;

XX

DT 21-AUG-1996 (first entry)

XX

DE Human CRF receptor A1 cDNA.

XX

KW Corticotropin releasing factor receptor; CRF-R; corticoliberin;

KW signal transduction; db.

XX Homo sapiens.
 XX OS
 XX Key Location/Qualifiers
 XX CDS 89..1329
 XX FT /*tag= a
 XX MO9617934-A2.
 XX 13-JUN-1996.
 XX 06-DEC-1995; 95WO-US015909.
 XX 09-DEC-1994; 94US-00353537.
 XX 17-JAN-1995; 95US-00374009.
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 XX Perrin MH, Chen R, Lewis KA, Vale MW, Donaldson CJ, Sawchenko P;
 XX WPI; 1996-287179/29.
 XX P-PSDB; AAR97290.
 XX Isolated corticotropin-releasing factor receptor (CRF-R) - used to
 XX develop prods. for modulating signal transduction activity mediated by
 XX CRF-R.
 XX Claim 6; Page 75-77; 102pp; English.
 XX A cDNA clone (AAR28968), designated CRF-R1, codes for a new G-protein-
 XX coupled receptor protein (AAR97290), which has high binding affinity for
 XX corticotropin releasing factor (CRF). It was isolated from a cDNA library
 XX prep'd. from human pituitary corticotrope adenoma (Cushing's tumour) by
 XX screening using an expression cloning approach; a splice variant (see
 XX AAR28969) was also identified. The cDNA can be used as a probe for
 XX detecting the presence of CRF receptor-encoding nucleic acids in samples
 XX or for the identification of additional CRF receptors, or can be used for
 XX prodn. of recombinant CRF receptor, or in gene therapy to target a vector
 XX to specific cell types
 XX SQ Sequence 1495 BP; 271 A; 496 C; 403 G; 325 T; 0 U; 0 Other;
 Query Match 88.4%; Score 1398; DB 2; Length 1495;
 Best Local Similarity 94.5%; Pred. No. 0;
 Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;
 QY 1 CGAGCCGCGAGCCGCGCGGTTCTCTGGGATGTCCTAGGACCCGCGCATTCAGGAC 60
 DB 1 CGAGCCGCGAGCCGCGCGGTTCTCTGGGATGTCCTAGGACCCGCGCATTCAGGAC 60
 QY 61 GGTAGCCGAGCGCGCGGATGGGAGGACCCCGAGCTCCGTCTCGTCAAGGCCCTT 120
 DB 61 GGTAGCCGAGCGCGCGGATGGGAGGACCCCGAGCTCCGTCTCGTCAAGGCCCTT 120
 QY 121 CTCCTCTGCGGCTGAACCCCGTCTCTGCTCCCTCCAGACCCAGCACTCCGAGAGCCTG 180
 DB 121 CTCCTCTGCGGCTGAACCCCGTCTCTGCTCCCTCCAGACCCAGCACTCCGAGAGCCTG 180
 QY 181 TCCTGCGCCAGCAACATCTCAGGACTGCACTGCAAGCAAGCATCCGTGGACCTCATTCGAC 240
 DB 181 TCCTGCGCCAGCAACATCTCAGGACTGCACTGCAAGCAAGCATCCGTGGACCTCATTCGAC 240
 QY 241 TGTGCGCCGCGAGCCCTGCGGGGACGTAGTGGTTGCGGCCCTGCCCTTTTCTAT 300
 DB 241 TGTGCGCCGCGAGCCCTGCGGGGACGTAGTGGTTGCGGCCCTGCCCTTTTCTAT 300
 QY 301 GGTGTCCGTACAAATACCAAAATGGCTACCGGAGTGCTTGGCCAAATGGCAGCTGG 360
 DB 301 GGTGTCCGTACAAATACCAAAATGGCTACCGGAGTGCTTGGCCAAATGGCAGCTGG 360
 QY 361 GCGCCGCGGTGAATTAATCTCCGAGTGCAGGAGATCTCAATGAGGAGAAAAAAGCAAG 420
 DB 361 GCGCCGCGGTGAATTAATCTCCGAGTGCAGGAGATCTCAATGAGGAGAAAAAAGCAAG 420

QY 421 GTGCACTACCATGTGCGAGTCAATCAACTACCTGGGCCACTGTATCTCCCTGGTGGCC 480
 DB 421 GTGCACTACCATGTGCGAGTCAATCAACTACCTGGGCCACTGTATCTCCCTGGTGGCC 480
 QY 481 CTCTGCTGGCTTTGTCTCTTTTGTGGGCTCAGGCGAGGCTGCACCAATTTGGGGTGAC 540
 DB 481 CTCTGCTGGCTTTGTCTCTTTTGTGGGCTC----- 513
 QY 541 CAGGAGATGGAGCCCTCGAGGTGGGGGCTCCATGGAGTGGTGGCCCATTTTCAGGTTGGA 600
 DB 514 ----- 513
 QY 601 AGGAGCATCCGGTGCCTGGAAACATCATCTACTGGAACTCATCTCCGCTTTCATCTCTG 660
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 QY 661 CGCAACGCCACCTGGTTCTGTGTCAGCTAAACCATGAGCCCGAGGTCCACAGAGCAAC 720
 DB 574 CGCAACGCCACCTGGTTCTGTGTCAGCTAAACCATGAGCCCGAGGTCCACAGAGCAAC 633
 QY 721 GTGGGCTGTGCAAGTTGTGTGACAGCCGCTACAACTACTTCCATGTGACCAACTTCTTC 780
 DB 634 GTGGGCTGTGCAAGTTGTGTGACAGCCGCTACAACTACTTCCATGTGACCAACTTCTTC 693
 QY 781 TGGATGTTCCGGGAGGGCTGTACTGTGCACACAGCCATCGTGTCTCACCTACTCCACTGAC 840
 DB 694 TGGATGTTCCGGGAGGGCTGTACTGTGCACACAGCCATCGTGTCTCACCTACTCCACTGAC 753
 QY 841 CGGCTCGCAATGGATGTTCTATCTGTGCTGGGGTGTGCCCTTCCCAATCATTTGTG 900
 DB 754 CGGCTCGCAATGGATGTTCTATCTGTGCTGGGGTGTGCCCTTCCCAATCATTTGTG 813
 QY 901 GCTTGGGCAATTGGGAAGCTGTACTAGCAATAGAGAAGTGTGTTGGCAAAAGGCTT 960
 DB 814 GCTTGGGCAATTGGGAAGCTGTACTAGCAATAGAGAAGTGTGTTGGCAAAAGGCTT 873
 QY 961 GGGGTGTACACCGACTACATCTACCAAGGCGCCCATCATCTCTGTCTCTGTGATCAATTC 1020
 DB 874 GGGGTGTACACCGACTACATCTACCAAGGCGCCCATCATCTCTGTCTCTGTGATCAATTC 933
 QY 1021 ATCTTCTTTTCAACATCGTCCGCACTCTCATGACCAAGCTCCGGGCATCCACCAAGTCT 1080
 DB 934 ATCTTCTTTTCAACATCGTCCGCACTCTCATGACCAAGCTCCGGGCATCCACCAAGTCT 993
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 DB 994 GAGACCAATTCAGTACAGGAAGGCTGTGAAAAGCCTCTGTGTCTGTCTGCCCTCTCTGGGC 1053
 QY 1141 ATCACCCTACATGCTGTTCTTGTCAATCCCGGGAGGATGAGTCTCCCGGGTCTGTTTC 1200
 DB 1054 ATCACCCTACATGCTGTTCTTGTCAATCCCGGGAGGATGAGTCTCCCGGGTCTGTTTC 1113
 QY 1201 ATCTACTTCAACTCTCTTCTGGAATCTTTCCAGGGCTTCTTTGTGTCTGTGTTCTACTGT 1260
 DB 1114 ATCTACTTCAACTCTCTTCTGGAATCTTTCCAGGGCTTCTTTGTGTCTGTGTTCTACTGT 1173
 QY 1261 TTCCTCAATAGTAGAGTCCGTTCTGCATCCGGAAGAGGTGGCACCCGGTGGCAGGACAAG 1320
 DB 1174 TTCCTCAATAGTAGAGTCCGTTCTGCATCCGGAAGAGGTGGCACCCGGTGGCAGGACAAG 1233
 QY 1321 CACTCGATCCGTGCCGAGTGGCCGCTGCTCATCCCTCCACCTCCCAACCCGCTGTC 1380
 DB 1234 CACTCGATCCGTGCCGAGTGGCCGCTGCTCATCCCTCCACCTCCCAACCCGCTGTC 1293
 QY 1381 AGCTTTTCAAGCATCAAGCAGTCCACAGAGTCTGAGCTGGCAGGTCTATGGAGCAAGCC 1440
 DB 1294 AGCTTTTCAAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCTATGGAGCAAGCC 1353
 QY 1441 CAAAGAGCTGTGGCTGGGGGAGTACGGCCAGGCTCCCTGACCACTCCCTGCTGTGAGGT 1500
 DB 1354 CAAAGAGCTGTGGCTGGGGGAGTACGGCCAGGCTCCCTGACCACTCCCTGCTGTGAGGT 1413

QY 1501 GACCTGTAGGCTCTATGCCCACTCCCGAGGAGGAGCTGGCACTGACAGCCTGGGGGG 1560
Db 1414 GACCTGTAGGCTCTATGCCCACTCCCGAGGAGGAGCTGGCACTGACAGCCTGGGGGG 1473
QY 1561 CCGCTCTCCCGCTGCGAGCCGTG 1582
Db 1474 CCGCTCTCCCGCTGCGAGCCGTG 1495

RESULT 7

AAD44482

ID AAD44482 standard; cDNA; 1495 BP.

XX AAD44482;

XX 13-DEC-2002 (first entry)

XX Human CRP-RA1 cDNA.

XX Human; G protein-coupled corticotropin-releasing factor receptor; CRF;

KW CRP-R; adrenocorticotrophic hormone; irritable bowel syndrome; therapy;

KW Cushing's syndrome; pituitary tumour; chronic stress; anorexia nervosa;

KW receptor; alcoholism; CRP-RA1; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FH 82..1329

FT CDS /*tag= a

FT /product= "hCRP-RA1 protein"

FT US200205617-A1.

XX 09-MAY-2002.

XX 12-NOV-1998; 98US-00191724.

XX 18-JUN-1993; 93US-00079320.

PR 23-AUG-1993; 93US-00110286.

PR 25-MAY-1994; 94WO-US005908.

PR 09-DEC-1994; 94US-00353537.

PR 07-JUN-1995; 95US-00483139.

XX (PERR/) PERRIN M H.

PA (CHEN/) CHEN R.

PA (LEWIS/) LEWIS K A.

PA (VALE/) VALE W W.

PA (DONA/) DONALDSON C J.

PA (SAWC/) SAWCHENKO P.

XX Perrin MH, Chen R, Lewis KA, Vale WW, Donaldson CJ, Sawchenko P;

XX WPI: 2002-462916/49.

XX P-PSDB; AAE26679.

XX New isolated recombinant mammalian G protein-coupled corticotropin-

PT releasing factor receptor protein for treating e.g. Cushing's syndrome,

PT pituitary tumors, stress, anorexia, alcoholism or irritable bowel

PT syndrome.

XX Claim 1; Page 20-22; 44pp; English.

XX The invention relates to recombinant mammalian G protein-coupled

CC corticotropin-releasing factor (CRF) receptor (CRF-R) proteins having

CC high affinity for CRF and nucleic acid molecules encoding such receptor

CC proteins. Polypeptides of the invention can be used to reduce high levels

CC of adrenocorticotrophic hormone caused by excess CRF and so can be used

CC to treat diseases such as Cushing's syndrome, pituitary tumours, chronic

CC stress, anorexia nervosa, alcoholism and irritable bowel syndrome. They

CC are used in pharmaceuticals and in the production of antibodies. The

CC present sequence is human CRP-RA1 cDNA

XX Sequence 1495 BP; 271 A; 496 C; 403 G; 325 T; 0 U; 0 Other;

Query Match 88.4%; Score 1398; DB 6; Length 1495;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 1 CGAGCCCGCAGCCGCGCGGTTCTCTGGGATGTCCTAGGACCCGGGCACTTCAAGGAC 60
Db 1 CGAGCCCGCAGCCGCGCGGTTCTCTGGGATGTCCTAGGACCCGGGCACTTCAAGGAC 60
QY 61 GGTAGCCGAGCGAGCCCGGAGGATGGAGGGCACTCCGAGCTCCGTCTCGTCAAGGCCCTT 120
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QY 121 CTCCTTCTGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCCGAGCACTCGGAGGCTG 180
Db 121 CTCCTTCTGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCCGAGCACTCGGAGGCTG 180
QY 181 TCCCTGGCCAGCAATCTCAGGACTGCAAGCAATGGCTCAAGCACTCCGTGACCTCATTTGGCACC 240
Db 181 TCCCTGGCCAGCAATCTCAGGACTGCAAGCAATGGCTCAAGCACTCCGTGACCTCATTTGGCACC 240
QY 241 TGCTGGCCCGCAGCCCTCGGGGAGCTAGTGGTTTCGGCCCTGCGCTGCTTTTCTAT 300
Db 241 TGCTGGCCCGCAGCCCTCGGGGAGCTAGTGGTTTCGGCCCTGCGCTGCTTTTCTAT 300
QY 301 GGTGTCGCTACAAATACCAAAATGGCTACCGGGAGTGCCTGGCCAAATGGCAGCTGG 360
Db 301 GGTGTCGCTACAAATACCAAAATGGCTACCGGGAGTGCCTGGCCAAATGGCAGCTGG 360
QY 361 GCGCCCGCGTGAAATTTACTCCGAGTCCAGGAGTCTCAATGAGGAGAAAAAAGCAAG 420
Db 361 GCGCCCGCGTGAAATTTACTCCGAGTCCAGGAGTCTCAATGAGGAGAAAAAAGCAAG 420
QY 421 GTGCACTACATGTGCGAGTCAATCAACTACTCGGGCCACTGTATCTCCCTGGTGCC 480
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QY 481 CTCCTGGTGCGCTTTGTCTCTTTCTGGGCTCAGGCCAGGCTGCACCCATTTGGGGTGAC 540
Db 481 CTCCTGGTGCGCTTTGTCTCTTTCTGGGCTCAGGCCAGGCTGCACCCATTTGGGGTGAC 540
QY 541 CAGGCAGATGGAGCCCTCGGAGGTGGGGCTCCATGAGTGGTGCCCAATTTCAAGTTTCCA 600
Db 541 ----- 513
QY 601 AGGAGCATCCGGTGCCTGGGAAACATCATCTCACTGGAACTCATCTCCGCTTCACTCTG 660
Db 514 AGGAGCATCCGGTGCCTGGGAAACATCATCTCACTGGAACTCATCTCCGCTTCACTCTG 573
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Db 574 CGCAACGCCACCTGGTTCCGTGCTCCAGTAAACCATGAGCCCGGAGGTCCACAGAGCAAC 633
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Db 634 GTGGGCTGGTGCAAGTTGGTGACAGCGGCTCAACTACTTCCATCTGACCAACTCTTTC 693
QY 781 TGGATCTTCCGGGAGGGCTGTACTCTGCACACAGCCATCGTGTCTCACTACTCCACTGAC 840
Db 694 TGGATCTTCCGGGAGGGCTGTACTCTGCACACAGCCATCGTGTCTCACTACTCCACTGAC 753
QY 841 CGGCTCGCAATATGATTTCACTCTGCAATGGCTGGGGTGTGCCCTTCCCACTCATTTGTG 900
Db 754 CGGCTCGCAATATGATTTCACTCTGCAATGGCTGGGGTGTGCCCTTCCCACTCATTTGTG 813
QY 901 GCTTGGGCAATTTGGGAGCTGTACTACGCAATGAGAGTGTGGTTTGGCAAAAGGCTT 960
Db 814 GCTTGGGCAATTTGGGAGCTGTACTACGCAATGAGAGTGTGGTTTGGCAAAAGGCTT 873
QY 961 GGGGTGTACACCGACTACATCTACAGGGGCCCATGATCTCGTCTCTGTGATCAATTTTC 1020
Db 874 GGGGTGTACACCGACTACATCTACAGGGGCCCATGATCTCGTCTCTGTGATCAATTTTC 933

```
QY 1021 ATCTTCCTTTTCAACATCGTCGCGATCCTCATGACCAAGCTCCGGGCATCCACCAAGTCT 1080
Db 934 ATCTTCCTTTTCAACATCGTCGCGATCCTCATGACCAAGCTCCGGGCATCCACCAAGTCT 993
QY 1081 GAGACCAATTAGTACAGAAAGGTGTGAAGGCACTCTGTGTGTGTGTGCCCCCTCTGGGC 1140
Db 994 GAGACCAATTAGTACAGAAAGGTGTGAAGGCACTCTGTGTGTGTGTGCCCCCTCTGGGC 1053
QY 1141 ATCACTTACATGCTGTCTTCTGTCATCCCGGGGAGGATGAGTCTCCCGGTCTCTTC 1200
Db 1054 ATCACTTACATGCTGTCTTCTGTCATCCCGGGGAGGATGAGTCTCCCGGTCTCTTC 1113
QY 1201 ATCTACTTCAACTCTCTCTGGAACTCTTCAGGGCTCTTTGTGTGTGTGTGTCTACTGT 1260
Db 1114 ATCTACTTCAACTCTCTCTGGAACTCTTCAGGGCTCTTTGTGTGTGTGTGTCTACTGT 1173
QY 1261 TTCTCTCAATAGTGTGCTCTTCTGTCATCCGGAAGAGGTGGCACTGGTGGCAGGCAAG 1320
Db 1174 TTCTCTCAATAGTGTGCTCTTCTGTCATCCGGAAGAGGTGGCACTGGTGGCAGGCAAG 1233
QY 1321 CACTCGATCCGTCCCGAGTGGCCGCTGTCATCCCACTCCCACTCCCACTCCCACTCCCACT 1380
Db 1234 CACTCGATCCGTCCCGAGTGGCCGCTGTCATCCCACTCCCACTCCCACTCCCACTCCCACT 1293
QY 1381 AGCTTTCAAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCTATGGAGCAGCCCC 1440
Db 1294 AGCTTTCAAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCTATGGAGCAGCCCC 1353
QY 1441 CAAAGAGCTGTGCTGGGGGATGACGGCCAGGCTCCCTGACCACTCCCTGCTGTGAGGT 1500
Db 1354 CAAAGAGCTGTGCTGGGGGATGACGGCCAGGCTCCCTGACCACTCCCTGCTGTGAGGT 1413
QY 1501 GACCTGTAGTCTCATGCCCACTCCCGCAGGAGCAGTGGCACTGACAGCTTGGGGGG 1560
Db 1414 GACCTGTAGTCTCATGCCCACTCCCGCAGGAGCAGTGGCACTGACAGCTTGGGGGG 1473
QY 1561 CCGCTCTCCCTGACGCGTG 1582
Db 1474 CCGCTCTCCCTGACGCGTG 1495
```

RESULT 8

```
ABX93034
ID ABX93034 standard; cDNA; 1495 BP.
XX
AC ABX93034;
XX
XX
XX 21-MAY-2003 (first entry)
XX Human corticotropin-releasing factor receptor 1 (CRF-R1) cDNA.
XX Human; gene; ss; corticotropin-releasing factor receptor; CRF;
XX G protein-coupled corticotropin-releasing factor receptor;
XX hypothalamic peptide; pituitary adrenocorticotrophic hormone; ACTH;
XX adrenal glucocorticoid; gene therapy; cortisol; Alzheimer's disease;
XX Cushing's disease; anorexia nervosa; alcoholism; anti-inflammatory;
XX irritable bowel syndrome; melancholic depression; neuroprotective;
XX neotropic; antidepressant.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 82..1329
XX /*tag= a
XX /*product= "CRF-R1"
XX
XX US6495343-B1.
XX
XX 17-DEC-2002.
XX
XX 17-JAN-1995; 95US-00374009.
XX
XX 18-JUN-1993; 93US-00079320.
XX
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PR 23-AUG-1993; 93US-00110286.
PR 25-MAY-1994; 94WO-US005908.
PR 09-DEC-1994; 94US-00353537.
XX
XX (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
XX Perrin MH, Chen R, Lewis KA, Vale WW, Donaldson CJ, Sawchenko P;
XX WPI; 2003-327461/31.
XX P-PSDB; AB08075.
XX
XX New nucleic acid and its encoded G protein-coupled corticotropin-
XX releasing factor receptor, useful for diagnosing or treating e.g. ACTH
XX levels or high cortisol levels associated with Alzheimer's disease or
XX Cushing's disease.
XX
XX Example 1; Col 37-40; 42pp; English.
XX
XX The invention discloses an isolated nucleic acid, which encodes a
XX mammalian G protein-coupled corticotropin-releasing factor (CRF) receptor
XX protein. CRF is a hypothalamic peptide which stimulates the secretion and
XX biosynthesis of pituitary adrenocorticotrophic hormone (ACTH) leading to
XX increased adrenal glucocorticoid production. The nucleic acid, or the CRF
XX receptor that it encodes, is useful in bioassays. The nucleic acid or CRF
XX receptor is particularly useful for providing recombinant receptors that
XX allows the development of less expensive, more sensitive and automated
XX means for assaying CRF and CRF-like compounds and developing CRF-based
XX therapeutics. The nucleic acid, or fragments of its encoded receptor, are
XX useful in therapy, e.g. gene therapy for reducing ACTH levels or treating
XX high cortisol levels associated with Alzheimer's diseases, Cushing's
XX diseases, anorexia nervosa, alcoholism or irritable bowel syndrome. These
XX are also useful in diagnostic assays, e.g. for diagnosing Alzheimer's
XX diseases, melancholic depression, anorexia nervosa, Cushing's diseases or
XX alcoholism. The sequence presented is the human CRF-R1 cDNA
XX
XX Sequence 1495 BP; 271 A; 496 C; 403 G; 325 T; 0 U; 0 Other;
```

```
Query Match 88.4%; Score 1398; DB 8; Length 1495;
Best Local Similarity 94.5%; Pred. NO. 0;
Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 1 CGAGCCCGCAGCGCCCGCGGTTCTCTGGAGTGTCCGTAGGACCCGGGCATTCAGGAC 60
Db 1 CGAGCCCGCAGCGCCCGCGGTTCTCTGGAGTGTCCGTAGGACCCGGGCATTCAGGAC 60
QY 61 GGTAGCCGAGCGAGCCCGGAGGATGGAGGGGACCCCGAGCTCGTCTCTCAAGGCCCTT 120
Db 61 GGTAGCCGAGCGAGCCCGGAGGATGGAGGGGACCCCGAGCTCGTCTCTCAAGGCCCTT 120
QY 121 CTCCTTCTGGGCTGAACCCCGTCTCTCCAGGACCCAGCACTGGAGAGCCCTG 180
Db 121 CTCCTTCTGGGCTGAACCCCGTCTCTCCAGGACCCAGCACTGGAGAGCCCTG 180
QY 181 TCCTGCGCCAGCAACATCTCAGGACTGCAAGTGCAGCATCCGTGGACCTCATTTGGCACC 240
Db 181 TCCTGCGCCAGCAACATCTCAGGACTGCAAGTGCAGCATCCGTGGACCTCATTTGGCACC 240
QY 241 TGTGCCCCCGCAGCCCTCGCGGGCAGCTAGTGTGTTGGGCCCTGCCCTCTTTTCTAT 300
Db 241 TGTGCCCCCGCAGCCCTCGCGGGCAGCTAGTGTGTTGGGCCCTGCCCTCTTTTCTAT 300
QY 301 GGTGTCGGCTACAAATACCAACAAATGGCTACCGGGAGTGCCTGGCCCAATGGCAGCTGG 360
Db 301 GGTGTCGGCTACAAATACCAACAAATGGCTACCGGGAGTGCCTGGCCCAATGGCAGCTGG 360
QY 361 GCGCCCGCGGTGAATTTACTCCGAGTCCAGGAGATCTCAATGAGGAGAAAAAGCAAG 420
Db 361 GCGCCCGCGGTGAATTTACTCCGAGTCCAGGAGATCTCAATGAGGAGAAAAAGCAAG 420
QY 421 GTGCACTACCATGTGCGAGTCATCAACTACCTGGGCCACTGTATCTCCCTGGTGGCC 480
Db 421 GTGCACTACCATGTGCGAGTCATCAACTACCTGGGCCACTGTATCTCCCTGGTGGCC 480
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QY 481 CTCTGGTGGCTTGTCTCTTCTGCGGCTCAGGCCAGGCTGCACCCATTGGGGTGAC 540
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Db 574 CGCAAGCCACCTGGTTCGCGGTCCAGTAAACATGAGCCCGAGGTCCACACAGAGCAAC 633
QY 721 GTGGGCTGGTGCAGGTTGGTGACAGCGCGCTCAACAATCTTCCATGTGACCAACTTCTTC 780
Db 634 GTGGGCTGGTGCAGGTTGGTGACAGCGCGCTCAACAATCTTCCATGTGACCAACTTCTTC 693
QY 781 TGGATGTTGGCGAGGGCTGCTACCTGCAACAGCCCATGCTGTCACTACTCCACTGAC 840
Db 694 TGGATGTTGGCGAGGGCTGCTACCTGCAACAGCCCATGCTGTCACTACTCCACTGAC 753
QY 841 CGGCTGGCAAAATGGATGTTTCATCTGCAATGGGCTGGGCTGCCCTCCCATCATCTGTG 900
Db 754 CGGCTGGCAAAATGGATGTTTCATCTGCAATGGGCTGGGCTGCCCTCCCATCATCTGTG 813
QY 901 GCCTGGGCCAATGGGAAGCTGTACTAGCAATGAGAGTGTGGTTTGGCAAAAGGCT 960
Db 814 GCCTGGGCCAATGGGAAGCTGTACTAGCAATGAGAGTGTGGTTTGGCAAAAGGCT 873
QY 961 GGGGTGTACACCGACTACATCTACAGGGGCCCATGATCTCTGCTGTGATCAATTTTC 1020
Db 874 GGGGTGTACACCGACTACATCTACAGGGGCCCATGATCTCTGCTGTGATCAATTTTC 933
QY 1021 ATCTCTCTTTTCAACATCGTCCGATCTCATGACCAAGTCTCGGGGATCACCACGCTCT 1080
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QY 1081 GAGACATTCAGTACAGAGAGGCTGTGAAGCCACTCTGCTGTGCTGCCCTCTCTGGGC 1140
Db 994 GAGACATTCAGTACAGAGAGGCTGTGAAGCCACTCTGCTGTGCTGCCCTCTCTGGGC 1053
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Db 1354 CAAAGAGCTGTGGTGGGGGATGACGGCCAGGCTCCCTGACCACTGCTGTGAGGT 1413
QY 1501 GACTGTGTAGGTCTCATGCCCACTCCCGCCAGGAGCAGTGGCATGACAGCTGGGGGGG 1560
Db 1414 GACTGTGTAGGTCTCATGCCCACTCCCGCCAGGAGCAGTGGCATGACAGCTGGGGGGG 1473
QY 1561 CGGCTCTCCCGCTGCAGCCGTG 1582

Db 1474 CGGCTCTCCCGCTGCAGCCGTG 1495

RESULT 9

ABX11833

ID ABX11833 standard; cDNA; 1495 BP.

XX ABX11833;

DT 07-MAY-2003 (first entry)

XX Human cDNA encoding corticotropin releasing factor receptor, hCRF-RA1.

XX Human; ss; gene; corticotropin releasing factor receptor; hCRF-RA1;
Cushing's disease; pituitary tumour; Alzheimer's disease;
melancholic depression; anorexia nervosa; chronic stress; alcoholism;
hypercortisolemia; gastrointestinal disorder; irritable bowel syndrome;
pre-eclampsia; pregnancy-induced complication; arthritis; abortion;
twinning.

XX Homo sapiens.

XX Key Location/Qualifiers
CDS 82..1329
/*tag= a
/product= "hCRF-RA1"

XX US6482608-B1.

XX 19-NOV-2002.

XX 26-MAY-2000; 2000US-00580734.

XX 18-JUN-1993; 93US-00079320.

XX 23-AUG-1993; 93US-00110286.

XX 25-MAY-1994; 94WO-05005908.

XX 09-DEC-1994; 94US-00353537.

XX 17-JAN-1995; 95US-00374009.

XX 12-JUN-1995; 95US-00483139.

XX 12-NOV-1998; 98US-00191724.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

XX Perrin MH, Chen R, Lewis KA, Vale MW, Donaldson CJ, Sawchenko P;

XX WPI; 2003-287359/28.

XX P-PSDB; ABG76046.

XX Novel cell line expressing nucleic acid expression vector comprising
nucleic acid encoding human corticotropin releasing factor (CRF) receptor
useful for reducing high adrenocorticotropin hormone, by binding to CRF.

XX Example 1; Col 37-40; 42pp; English.

XX The invention relates to a cell line expressing a recombinant
corticotropin releasing factor receptor (CRF-R) encoded by a nucleic acid
expression vector, or a cell line containing a nucleic acid vector
encoding a recombinant CRF-R. The vector encodes human CRF-R, subtype A,
variant 1 (hCRF-RA1). Also included is expressing a recombinant CRF
receptor in a suitable host cell, by expressing the vector, where the
nucleic acid encodes CRF-R that binds CRF or nucleic acid degenerate to
the naturally occurring nucleic acid. The cell line is useful for
expressing hCRF-RA1 protein by recombinant techniques and in binding
assays using CRF-R which are used for rapidly screening large number of
compounds to determine which compounds are capable of binding to CRF-R,
and for identifying new CRF-like ligands. The polypeptides expressed by
the cell line inhibit CRF binding to CRF-R and can inhibit CRF-induced
adrenocorticotropin hormone (ACTH) release in vitro by several cells, and
so are useful for reducing high ACTH levels caused by excess CRF, and for
treating Cushing's disease, pituitary tumours, Alzheimer's disease,
melancholic depression, anorexia nervosa, chronic stress, alcoholism and
hypercortisolemia. The proteins are also useful for treating

CC gastrointestinal disorders such as irritable bowel syndrome,
CC abnormalities such as pre-eclampsia, which occur during pregnancy, to
CC reduce pregnancy-induced complications and increased CRF levels which can
CC otherwise result in excessive release of ACTH. The proteins are also
CC useful for locally treating arthritis and other similar ailments,
CC modulating action of CRF in mammals, treating the pregnancy-related
CC pathological disorders in mammals. The CRF-R polypeptides are used in
CC such areas as the diagnosis and/or treatment of CRF-dependent tumours,
CC enhancing the survival of brain neurons, inducing abortion in livestock
CC and other domesticated animals, inducing twinning in livestock and other
CC domesticated animals. The present sequence encodes corticotropin
CC releasing factor receptor, hCRP-RAI
XX

Query Match 88.4%; Score 1398; DB 9; Length 1495;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 1 CGAGCCGACGAGCCGCGCGGTTCTCTGGGATGTCGAGACCCGGGCATTCAGGAC 60
DB 1 CGAGCCGACGAGCCGCGCGGTTCTCTGGGATGTCGAGACCCGGGCATTCAGGAC 60
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DB 61 GGTAGCGAGCGAGCCGCGGATGGAGGCGACCCCGAGCTCCGTCCTCAAGGCCCTT 120
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DB 181 TCCTGGCCAGCAACATCTCAGAGCTGCAAGCGATCCGTCGAGCCTCAATGGCACC 240
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QY 421 GTGCACTACCAATGTGGCAGTCATCACTACCTTGGGCCACTGTATCTCCCTGGTGGCC 480
DB 421 GTGCACTACCAATGTGGCAGTCATCACTACCTTGGGCCACTGTATCTCCCTGGTGGCC 480
QY 481 CTCCTGTGTCCTTTGTCCTTTCTGCGGCTAGGCGGCTGACCCCATTTGGGTGAC 540
DB 481 CTCCTGTGTCCTTTGTCCTTTCTGCGGCTC----- 513
QY 541 CAGGCAGATGGACCCCTGGAGGTGGGGCTCCATGGAGTGGTCCCATTTTCAGTTGCA 600
DB 514 ----- 513
QY 601 AGGAGCATCCGGTGCTCGGAAACATCATCCACTGGAACTCATCTCCGCTTTCATCCTG 660
DB 514 AGGAGCATCCGGTGCTCGGAAACATCATCCACTGGAACTCATCTCCGCTTTCATCCTG 573
QY 661 CGCAAACGCACTGGTGTGGTGTGTCAGCTAAACATGAGCCCGAGGTGCAACGAGCAAC 720
DB 574 CGCAAACGCACTGGTGTGGTGTGTCAGCTAAACATGAGCCCGAGGTGCAACGAGCAAC 633
QY 721 GTGGGCTGGTGAGGTGGTGACGCGCTCAACACTTCTTCCATGTGACCAACTCTTC 780
DB 634 GTGGGCTGGTGAGGTGGTGACGCGCTCAACACTTCTTCCATGTGACCAACTCTTC 693
QY 781 TGGATGTTCCGCGAGGCGCTCACTCTGCAACAGCCATCGTGTCACTCTCCACTGAC 840

DB 694 TGGATGTTCCGCGAGGCGTGTACCTGTGACACAGCCATCGTGTCACTACTCACTGAC 753
QY 841 CGGCTGGCAAAATGGATGTTCACTGTGATGGCTGGGTTGTCCTTCCCATCATTTG 900
DB 754 CGGCTGGCAAAATGGATGTTCACTGTGATGGCTGGGTTGTCCTTCCCATCATTTG 813
QY 901 GCTTGGGCCATTTGGGAAGCTGTACTACGAATAGAGAGTGTGGTTTGGCAAAAGCCCT 960
DB 814 GCTTGGGCCATTTGGGAAGCTGTACTACGAATAGAGAGTGTGGTTTGGCAAAAGCCCT 873
QY 961 GGGGTGTACACCGACTACATCTACCAAGGCCCATGATCCTGGTCTGTGTGATCAATTC 1020
DB 874 GGGGTGTACACCGACTACATCTACCAAGGCCCATGATCCTGGTCTGTGTGATCAATTC 933
QY 1021 ATCTTCTCTTTTCAACATCGTCCGCATCTCATGACCAAGCTCGGGCATCCACAGTCT 1080
DB 934 ATCTTCTCTTTTCAACATCGTCCGCATCTCATGACCAAGCTCGGGCATCCACAGTCT 993
QY 1081 GAGACCATTCAGTACAGGAAGCTGTGAAAGCCACTCTCGTGTCTGTGCTGCTTGGGC 1140
DB 994 GAGACCATTCAGTACAGGAAGCTGTGAAAGCCACTCTCGTGTCTGTGCTGCTTGGGC 1053
QY 1141 ATCACCTACATGCTGTCTTCTCAATCCCGGGAGGATGAGGTCTCCGGGTCTGCTTC 1200
DB 1054 ATCACCTACATGCTGTCTTCTCAATCCCGGGAGGATGAGGTCTCCGGGTCTGCTTC 1113
QY 1201 ATCTACTTCAACTCTTCTTGGAACTCTTCCAGGGCTTCTTGTGTGTGTCTACTGT 1260
DB 1114 ATCTACTTCAACTCTTCTTGGAACTCTTCCAGGGCTTCTTGTGTGTGTCTACTGT 1173
QY 1261 TTCTCTCAATAGTGTGAGTCCGTTCTGTCATCCGAAAGAGTGGCAAGGTGGCAGGACAAG 1320
DB 1174 TTCTCTCAATAGTGTGAGTCCGTTCTGTCATCCGAAAGAGTGGCAAGGTGGCAGGACAAG 1233
QY 1321 CACTCGATCCGTGCCGAGTGGCCCGTGCATGTCCATCCCACTTCCCAACCCCGTGTG 1380
DB 1234 CACTCGATCCGTGCCGAGTGGCCCGTGCATGTCCATCCCACTTCCCAACCCCGTGTG 1293
QY 1381 AGCTTTACAGCATCAGCAGTCCACAGCAGTCTGAGCTGGCAGGTTCATGGAGCAGCCCC 1440
DB 1294 AGCTTTACAGCATCAGCAGTCCACAGCAGTCTGAGCTGGCAGGTTCATGGAGCAGCCCC 1353
QY 1441 CAAAGAGCTGTGGCTGGGGGATGACGGCAGGCTCCCTGACCACTGCTGTGGAGGT 1500
DB 1354 CAAAGAGCTGTGGCTGGGGGATGACGGCAGGCTCCCTGACCACTGCTGTGGAGGT 1413
QY 1501 GACCTGTTAGGTCTCATGCCCCACTCCCCCAGGAGCAGTGGCACTGACAGCTGGGGGG 1560
DB 1414 GACCTGTTAGGTCTCATGCCACTCCCCCAGGAGCAGTGGCACTGACAGCTGGGGGG 1473
QY 1561 CGCTCTCTCCCTGCGAGCCGTG 1582
DB 1474 CGCTCTCTCCCTGCGAGCCGTG 1495
RESULT 10
ADJ65796
ID ADJ65796 standard; cDNA, 1495 BP.
XX
AC ADJ65796;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human corticotropin-releasing factor receptor CRF-RAI cDNA.
XX
KW Human; corticotropin-releasing factor receptor; CRF-RAI; ss; gene;
KW Alzheimer's disease; melancholic depression; anorexia nervosa;
KW Cushing's disease; hypercortisolemia; alcoholism;
KW gastrointestinal disorder; irritable bowel syndrome; inflammation;
KW Addison's disease; cardiac perfusion; blood pressure; hypotension.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
 FT CDS 82..1329
 FT /*tag= a
 FT /product= "CFR-RA1"
 XX
 XX US2004039173-A1.
 XX
 XX 26-FEB-2004.
 XX
 XX 26-AUG-2003; 2003US-00649193.
 XX
 XX 18-JUN-1993; 93US-00079320.
 XX 23-AUG-1993; 93US-00110286.
 XX 25-MAY-1994; 94WO-US0005908.
 XX 09-DEC-1994; 94US-00353537.
 XX 07-JUN-1995; 95US-00483139.
 XX 12-NOV-1998; 98US-00191724.
 XX
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 PA
 XX
 XX Perrin MH, Chen R, Lewis KA, Vale WW, Donaldson CJ, Sawchenko P;
 XX WPI; 2004-203293/19.
 XX P-PSDB; ADJ65797.
 XX
 XX New mammalian G protein-coupled corticotropin-releasing factor receptor
 PT protein, useful in diagnosing and treating Alzheimer's disease, anorexia
 PT nervosa, Cushing's disease, alcoholism, irritable bowel syndrome or
 PT hypotension.
 XX
 XX Example 1; SEQ ID NO 1; 44pp; English.
 XX
 CC The invention relates to an isolated mammalian G protein-coupled
 CC corticotropin-releasing factor (CRF) receptor protein or polypeptide from
 CC Rat, Mouse or human appearing as ADJ65801, ADJ65803, ADJ65805, or
 CC ADJ65810, encoded by the nucleic acids appearing as ADJ65800, ADJ65802,
 CC ADJ65804, or ADJ65809. Also included are a composition comprising CRF-R,
 CC an antibody generated against CRF-R and a diagnostic kit, for assaying
 CC for the presence in biological fluids of CRF-R protein, protein analogues
 CC and/or fragments, comprising CRF-R) and/or one or more antibodies. The
 CC protein, polynucleotide or composition is useful in diagnosing and
 CC treating Alzheimer's disease, melancholic depression, anorexia nervosa,
 CC Cushing's disease, hypercortisolemia or alcoholism, gastrointestinal
 CC disorders (e.g. irritable bowel syndrome) or physiological conditions
 CC (e.g. inflammation or Addison's disease), in regulating cardiac perfusion
 CC and in modulating blood pressure, thus combat hypotension. The present
 CC sequence encodes human CRF-RA1.
 XX
 XX Sequence 1495 BP; 271 A; 496 C; 403 G; 325 T; 0 U; 0 Other;
 SQ
 Query Match 88.4%; Score 1398; DB 12; Length 1495;
 Best Local Similarity 94.5%; Pred. No. 0;
 Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;
 QY 1 CGAGCCGCGAGCCGCGCGGTTCTCTGGGATGTCGTTAGACCCGCGGATTCAGGAC 60
 DB 1 CGAGCCGCGAGCCGCGCGGTTCTCTGGGATGTCGTTAGACCCGCGGATTCAGGAC 60
 QY 61 GGTAGCCGAGCGAGCCGCGGATGGGAGGACCCCGCAGCTCCGTCCTCGTCAAGGCCCTT 120
 DB 61 GGTAGCCGAGCGAGCCGCGGATGGGAGGACCCCGCAGCTCCGTCCTCGTCAAGGCCCTT 120
 QY 121 CTCTCTCTGGGGGTGAACCCCGTCTCTGCTCCCTCCAGGACCCAGCACTCGAGAGCCTG 180
 DB 121 CTCTCTCTGGGGGTGAACCCCGTCTCTGCTCCCTCCAGGACCCAGCACTCGAGAGCCTG 180
 QY 181 TCCTCTGCGCAGCAACATCTCAGGACTCAGTGCAGCAACGATCCGTTGGACCTCATTTGGCACC 240
 DB 181 TCCTCTGCGCAGCAACATCTCAGGACTCAGTGCAGCAACGATCCGTTGGACCTCATTTGGCACC 240
 QY 241 TGCTGGCCCGCAGCCCTGCGGGGACAGTGTGGTTCGGCCCTGCTCTTTTCTAT 300
 DB 241 TGCTGGCCCGCAGCCCTGCGGGGACAGTGTGGTTCGGCCCTGCTCTTTTCTAT 300

QY 301 GGTGTCCGCTACAATACCAAAACAATGGCTACCGGAGTGCCTGGCCAATGCGAGCTGG 360
 DB 301 GGTGTCCGCTACAATACCAAAACAATGGCTACCGGAGTGCCTGGCCAATGCGAGCTGG 360
 QY 361 GCGCCCGCGGTGAATTAATCTCCGAGTCCAGGAGATCCTCAATGAGGAGAAAAAAGCAAG 420
 DB 361 GCGCCCGCGGTGAATTAATCTCCGAGTCCAGGAGATCCTCAATGAGGAGAAAAAAGCAAG 420
 QY 421 GTGCACTACCATGTGCGAGTCAATCACTACCTGGGCCACCTGTATCTCCCTGGTGGCC 480
 DB 421 GTGCACTACCATGTGCGAGTCAATCACTACCTGGGCCACCTGTATCTCCCTGGTGGCC 480
 QY 481 CTCCTGGTGGCTTTGTCTCTTTCTGGGCTCAGGCGAGGTGCACCAATTTGGGGTGAC 540
 DB 481 CTCCTGGTGGCTTTGTCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 513
 QY 541 CAGGCAGATGGAGCCCTCGGAGGTGGGGGCTCCATGGAGTGGTGGCCCATTTCAAGTTTCCA 600
 DB 514 ----- 513
 QY 601 AGGAGCATCCGCTGCTCGGAAAACATCACTCACTGGAAACCTCATCTCGCCTTTCATCTG 660
 DB 514 AGGAGCATCCGCTGCTCGGAAAACATCACTCACTGGAAACCTCATCTCGCCTTTCATCTG 660
 QY 661 CGAACGCCACCTGGTTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 DB 574 CGAACGCCACCTGGTTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 633
 QY 721 GTGGGCTGGTGGCAGGTTGGTGACAGCGGCTCACTCACTTCTTCCATGTGACCACTTCTTC 780
 DB 634 GTGGGCTGGTGGCAGGTTGGTGACAGCGGCTCACTCACTTCTTCCATGTGACCACTTCTTC 693
 QY 781 TGGATGTTGGCGAGGGCTGCTACTGCTGCAACAGCCATCGTGTCTCACTACTCCACTGAC 840
 DB 694 TGGATGTTGGCGAGGGCTGCTACTGCTGCAACAGCCATCGTGTCTCACTACTCCACTGAC 753
 QY 841 CGGCTCGCAAAATGGAATGTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 DB 754 CGGCTCGCAAAATGGAATGTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 813
 QY 901 GCTTGGGCCCAATGGGAGCTGTACTAGCAATGAGAGTGTGCTTGGTGGCAAAAGGSCCT 960
 DB 814 GCTTGGGCCCAATGGGAGCTGTACTAGCAATGAGAGTGTGCTTGGTGGCAAAAGGSCCT 873
 QY 961 GGGGTGTACACCGACTACATCTACAGGGGCCCATGATCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 DB 874 GGGGTGTACACCGACTACATCTACAGGGGCCCATGATCTGCTGCTGCTGCTGCTGCTGCTGCT 933
 QY 1021 ATCTTCTTTTCAACATGCTCCGATCTCATGACCAAGCTCCGGGATCCACACGCTCT 1080
 DB 934 ATCTTCTTTTCAACATGCTCCGATCTCATGACCAAGCTCCGGGATCCACACGCTCT 993
 QY 1081 GAGACCAATTCAGTACAGGAGGCTGTGAAGCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 DB 994 GAGACCAATTCAGTACAGGAGGCTGTGAAGCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1053
 QY 1141 ATCACTCTACATGCTGTTCTTCTGCTCAATCCCGGGAGGATGAGGTCTCCCGGGTCTGCTTC 1200
 DB 1054 ATCACTCTACATGCTGTTCTTCTGCTCAATCCCGGGAGGATGAGGTCTCCCGGGTCTGCTTC 1113
 QY 1201 ATCTACTTCACTCTCTTCTGGAATCTTTCAGGGCTTCTTTGTTGTTGTTGTTGTTGTTGTTGTT 1260
 DB 1114 ATCTACTTCACTCTCTTCTGGAATCTTTCAGGGCTTCTTTGTTGTTGTTGTTGTTGTTGTTGTT 1173
 QY 1261 TTCTCTCAATGAGTCCGTTCTGTCATCCGGAAGAGTGGCAACCGTGGCGAGGCAAG 1320
 DB 1174 TTCTCTCAATGAGTCCGTTCTGTCATCCGGAAGAGTGGCAACCGTGGCGAGGCAAG 1233
 QY 1321 CACTCGATCCGTCGCCGAGTGGCCCGTGCATGTCCATCCCACTCCCACTCCCACTCCCACTCCCACT 1380
 DB 1234 CACTCGATCCGTCGCCGAGTGGCCCGTGCATGTCCATCCCACTCCCACTCCCACTCCCACTCCCACT 1293

QY 1381 AGCTTTTCACAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCAATGAGCAGCCCC 1440
Db 1294 AGCTTTTCACAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCAATGAGCAGCCCC 1353
QY 1441 CAAAGAGCTGTGGCTGGGGGATGACGGCCAGAGCTCCCTGACACCCCTGCTGTGAGGT 1500
Db 1354 CAAAGAGCTGTGGCTGGGGGATGACGGCCAGAGCTCCCTGACACCCCTGCTGTGAGGT 1413
QY 1501 GACCTGTTAGGTCTCATGCCCCACTCCCCCAGGAGCAGCTGGGCACTGACAGCCCTGGGGGGG 1560
Db 1414 GACCTGTTAGGTCTCATGCCCCACTCCCCCAGGAGCAGCTGGGCACTGACAGCCCTGGGGGGG 1473
QY 1561 CCGCTCTCCCCCTGCAGCCGTG 1582
Db 1474 CCGCTCTCCCCCTGCAGCCGTG 1495
RESULT 11
AAS62243/c
ID AAS62243 standard; cDNA; 2579 BP.
AC AAS62243;
XX AAS62243;
DT 14-FEB-2002 (first entry)
XX cDNA sequence #30 encoding novel human secreted protein.
DE Human secreted protein; hyperproliferative disorder; autoimmune disorder;
KW immune deficiency disorder; blood disorder; inflammatory disorder;
KW infectious disorder; gene therapy; antimicrobial; hepatotropic;
KW immunosuppressive; antirheumatic; ss.
XX Homo sapiens.
OS
XX
XX W0200177291-A2.
XX 18-OCT-2001.
XX 29-MAR-2001; 2001WO-US010485.
XX 06-APR-2000; 2000US-0195604P.
PR (GEMY) GENETICS INST INC.
XX
XX Wong GG, Clark HF, Fachtel K, Agostino MJ, Howes SH, Resnick RJ;
PI Gulukota K, Graham JR;
PI
XX WPI; 2002-010900/01.
XX New polynucleotides encoding secreted proteins useful for treating e.g.
PT asthma, HIV and Crohn's disease.
PT
XX
XX Claim 1; Page 86-87; 391pp; English.
PS
XX The present invention relates to the isolation of novel cDNA sequences
CC which encode human secreted proteins. The cDNA sequences have been
CC derived from a variety of human tissues. The invention also provides a
CC method for producing proteins from these polynucleotide sequences. The
CC proteins are useful for identifying compounds that modulate their
CC activity and production, and the cell is also useful for identifying
CC compounds that modulate expression of the polynucleotide sequences
CC encoding the secreted proteins. The sequences of the invention are useful
CC for treating diseases such as hyperproliferative disorders (e.g. cancer),
CC immune deficiency disorders (e.g. severe combined immunodeficiency
CC (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders
CC (e.g. thrombocytopenia), inflammatory disorders (e.g. arthritis) and
CC infectious disorders (e.g. hepatitis). The polynucleotide sequences of
CC the invention are also useful in gene therapy. AAS62214-AAS62838
CC represent the cDNA sequences of the invention that encode for novel human
CC secreted proteins
XX
SQ Sequence 2579 BP; 501 A; 733 C; 840 G; 505 T; 0 U; 0 Other;

Query Match 88.4%; Score 1398; DB 6; Length 2579;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;
QY 1 CQAGCCCGCAGCGCCGCGGTTCTCTGGGATGTCCGTAGGACCCCGGGCAATTGAGGAC 60
Db 2420 CQAGCCCGCAGCGCCGCGGTTCTCTGGGATGTCCGTAGGACCCCGGGCAATTGAGGAC 2361
QY 61 GGTAGCCGAGCCAGCCGAGGATGGAGGGGACCCGCGAGCTCCGTCTCGTCAAGGCCCTT 120
Db 2360 GGTAGCCGAGCCAGCCGAGGATGGAGGGGACCCGCGAGCTCCGTCTCGTCAAGGCCCTT 2301
QY 121 CTCCTTCTGGGCTGAACCCCGCTCTCTGCTCCCTCCAGGACCACTGCGAGAGCCCTG 180
Db 2300 CTCCTTCTGGGCTGAACCCCGCTCTCTGCTCCCTCCAGGACCACTGCGAGAGCCCTG 2241
QY 181 TCCCTGGCCAGCAACATCTCAGGACTGCGAGTGCACATCCGATCCGTGGAACCTCATTTGGCACC 240
Db 2240 TCCCTGGCCAGCAACATCTCAGGACTGCGAGTGCACATCCGATCCGTGGAACCTCATTTGGCACC 2181
QY 241 TGTGGCCCGCAGCCCTGCGGGGCGAGCTAGTGGTTGGGCCCTGCGCTGCTTTTCTAT 300
Db 2180 TGTGGCCCGCAGCCCTGCGGGGCGAGCTAGTGGTTGGGCCCTGCGCTGCTTTTCTAT 2121
QY 301 GGTGTCCGCTACATACCAACAAATGGCTACCGGGAGTGGCTTGGCCAAATGGCAGCTGG 360
Db 2120 GGTGTCCGCTACATACCAACAAATGGCTACCGGGAGTGGCTTGGCCAAATGGCAGCTGG 2061
QY 361 GCGCCCGCGGTGAATTACTCCAGTGGCAGGAGATCTCAATGAGAGAGAAAAAGCAAG 420
Db 2060 GCGCCCGCGGTGAATTACTCCAGTGGCAGGAGATCTCAATGAGAGAGAAAAAGCAAG 2001
QY 421 GTGCACTACCATGTGCGAGTCACTCAACTACTCTGGGCCACTGTATCTCCCTGGTGGCC 480
Db 2000 GTGCACTACCATGTGCGAGTCACTCAACTACTCTGGGCCACTGTATCTCCCTGGTGGCC 1941
QY 481 CTCCTGGTGGCCCTTTGTCTCTTTCTGGCGCTCAGGCCAGGCTGCACCCATTTGGGGTGAC 540
Db 1940 CTCCTGGTGGCCCTTTGTCTCTTTCTGCGGCTC----- 1908
QY 541 CAGGCAAGATGGAGCCCTGGAGGTGGGGGCTCCATGAGTGTGGTGGCCCAATTGAGTTGCA 600
Db 1907 ----- 1908
QY 601 AGGAGCATCCGGTGGCTGGGAACATCATCCACTGGAACTCATCTCCGCTTTCATCCG 660
Db 1907 AGGAGCATCCGGTGGCTGGGAACATCATCCACTGGAACTCATCTCCGCTTTCATCCG 1848
QY 661 CGCAACGCCACCTGGTTCTGGTCCAGCTAACACATGAGCCCGAGGTCCACAGAGCAAC 720
Db 1847 CGCAACGCCACCTGGTTCTGGTCCAGCTAACACATGAGCCCGAGGTCCACAGAGCAAC 1788
QY 721 GTGGGCTGTGAGGTGTGTGACAGCGGCTTAACTACTTCAATGTGACCAACTTCTTC 780
Db 1787 GTGGGCTGTGAGGTGTGTGACAGCGGCTTAACTACTTCAATGTGACCAACTTCTTC 1728
QY 781 TGGATGTTCCGGGAGGCTGCTACCTGACAGCCATCGTCTCACTTCCACTGAC 840
Db 1727 TGGATGTTCCGGGAGGCTGCTACCTGACAGCCATCGTCTCACTTCCACTGAC 1668
QY 841 CGGCTCGCAAAATGGAATGTTCACTGCAATGGCTGGGGTGTGCCCTTCCCCCATTTGTG 900
Db 1667 CGGCTCGCAAAATGGAATGTTCACTGCAATGGCTGGGGTGTGCCCTTCCCCCATTTGTG 1608
QY 901 GCTTGGGCCAATTGGGAAGCTGTACTACGACAAATGAGAAAGTGTGTTGGGCAAAAGCCCT 960
Db 1607 GCTTGGGCCAATTGGGAAGCTGTACTACGACAAATGAGAAAGTGTGTTGGGCAAAAGCCCT 1548
QY 961 GGGGTGTACACCGACTACATCTACAGGGGCCCAATGATCTCGTCTCTGATCAATTTC 1020
Db 1547 GGGGTGTACACCGACTACATCTACAGGGGCCCAATGATCTCGTCTCTGATCAATTTC 1488
QY 1021 ATCTTCTTTTCAACATCGTCCGCATCTCATGACCAAGCTCCGGGCATCCACACGTCT 1080

Db 1487 ATCTTCTTTTCAACATCGTCCGATCCTCATGACCAAGTCCGGGATCCACACGTCT 1428
Qy 1081 GAGACCAATTCAGTACAGGAAGGCTGTGAAGCCACATCTGTGTCTGTCTGCCCTCTCTGGGC 1140
Db 1427 GAGACCAATTCAGTACAGGAAGGCTGTGAAGCCACATCTGTGTCTGTCTGCCCTCTCTGGGC 1368
Qy 1141 ATCACTACATGCTGTTCTTCTGTCATCCCGGGAGGATGAGTCTCCGGGTCTGCTTC 1200
Db 1367 ATCACTACATGCTGTTCTTCTGTCATCCCGGGAGGATGAGTCTCCGGGTCTGCTTC 1308
Qy 1201 ATCTACTTCAACTCTTCTCGGAATCTTCCAGGGCTTCTTGTGTCTGTCTACTGT 1260
Db 1307 ATCTACTTCAACTCTTCTCGGAATCTTCCAGGGCTTCTTGTGTCTGTCTACTGT 1248
Qy 1261 TTCTCTCAATAGTGAAGTCCGTTCTGCCATCCGGAAGAGTGGCACCGGTGGCAGGACAAG 1320
Db 1247 TTCTCTCAATAGTGAAGTCCGTTCTGCCATCCGGAAGAGTGGCACCGGTGGCAGGACAAG 1188
Qy 1321 CACTCATCGTCCCGAGTGGCCGTCGTCATGTCATCCCACTTCCCAACCCGTC 1380
Db 1187 CACTCATCGTCCCGAGTGGCCGTCGTCATGTCATCCCACTTCCCAACCCGTC 1128
Qy 1381 AGCTTTACAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGTCAATGAGCAGCCCC 1440
Db 1127 AGCTTTACAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGTCAATGAGCAGCCCC 1068
Qy 1441 CAAAGAGCTGTGCTGGGGGATGACGGCCAGCGTCCCTGACCACTCCCTCTGTGAGGT 1500
Db 1067 CAAAGAGCTGTGCTGGGGGATGACGGCCAGCGTCCCTGACCACTCCCTCTGTGAGGT 1008
Qy 1501 GACCTGTAGTCTCATGCCCCTGAGGAGAGTGGGAGTGGGAGTGGGAGG 1560
Db 1007 GACCTGTAGTCTCATGCCCCTGAGGAGAGTGGGAGTGGGAGTGGGAGG 948
Qy 1561 CGGCTCTCCCGTCAGCGGTG 1582
Db 947 CGGCTCTCCCGTCAGCGGTG 926

RESULT 12
ID ADO29851
AC ADO29851;
XX ADO29851;
XX ADO29851;
DT 29-JUL-2004 (first entry)
XX Human GPCR CRHR1 polynucleotide, SEQ ID NO:953.
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
KW cytostatic; antiinflammatory; vasotropic; antiangiogenic; antirhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW viricide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW gene; ss.
XX
OS Homo sapiens.
XX
XX WO2004040000-A2.
XX
XX 13-MAY-2004.
XX
XX 09-SEP-2003; 2003WO-US028226.

XX 09-SEP-2002; 2002US-0409303P.
PR 09-APR-2003; 2003US-0461329P.
XX (PRIM-) PRIMAL INC.
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
XX WPI; 2004-390329/36.
DR P-PSDB; ADO29265.
XX Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX Claim 151; SEQ ID NO 953; 542pp; English.
XX The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridize to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
CC nucleic acid of the invention. Note: The full sequence data for this
CC patent did not form part of the printed specification; those sequences
CC not shown were obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2536 BP; 478 A; 836 C; 724 G; 498 T; 0 U; 0 Other;
Query Match 88.3%; Score 1396.4; DB 12; Length 2536;
Best Local Similarity 94.4%; Pred. No. 0;
Matches 1494; Conservative 0; Mismatches 1; Indels 87; Gaps 1;
Qy 1 CGAGCCCGCAGCGCCGCGGTCCTCTGGGATGTCGAGGACCCGGGCAATTCAGGAC 60
Db 146 CGAGCCCGCAGCGCCGCGGTCCTCTGGGATGTCGAGGACCCGGGCAATTCAGGAC 205
Qy 61 GGTAGCCGAGCGAGCCGAGGATGGAGGGCACCCCGAGCTCCGTCGTCAGGCCCTT 120
Db 206 GGTAGCCGAGCGAGCCGAGGATGGAGGGCACCCCGAGCTCCGTCGTCAGGCCCTT 265
Qy 121 CTCCTTCTGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCCAGCACTCGGAGGCTG 180
Db 266 CTCCTTCTGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCCAGCACTCGGAGGCTG 325
Qy 181 TCCCTGGCCAGCAACATCTCAGGACTGCGAGTCAAGCGCAATCCGTCGTCAGGCCCT 240
Db 326 TCCCTGGCCAGCAACATCTCAGGACTGCGAGTCAAGCGCAATCCGTCGTCAGGCCCT 385

241 TGCTGGCCCCGCGAGCCCTGCGGGGACAGCTAGTGGTTGCGCCCTGCCCCCTTTTCTAT 300
| | | | |
Db TGCTGGCCCCGCGAGCCCTGCGGGGACAGCTAGTGGTTGCGCCCTGCCCCCTTTTCTAT 445
| | | | |
QY 301 GGTGTCCGCTACAAATACCAAAATGGCTACCGGGAGTGCCTGGCCAATGGCAGCTGG 360
| | | | |
Db 446 GGTGTCCGCTACAAATACCAAAATGGCTACCGGGAGTGCCTGGCCAATGGCAGCTGG 505
| | | | |
QY 361 GCCGCCCGCTGAATTAATCCGAGTGCCAGGAGATCCTCAATGAGGAGAAAAAGCAAG 420
| | | | |
Db 506 GCCGCCCGCTGAATTAATCCGAGTGCCAGGAGATCCTCAATGAGGAGAAAAAGCAAG 565
| | | | |
QY 421 GTGCACTTACCAATGTGCGAGTCATCATCAACTACCTGGGCCACTGTATCTCCCTGGTGCC 480
| | | | |
Db 566 GTGCACTTACCAATGTGCGAGTCATCATCAACTACCTGGGCCACTGTATCTCCCTGGTGCC 625
| | | | |
QY 481 CTGCTGGTGCCCTTTGTCTCTTTCTGCGGCTGAGCCAGGCTGCACCCATTTGGGGTGAC 540
| | | | |
Db 626 CTGCTGGTGCCCTTTGTCTCTTTCTGCGGCTC----- 658
| | | | |
QY 541 CAGCGAGATGGAGCCCTGGAGGTGGGGCTCCATGGAGTGGTGCCTCCCATTTTCAGGTTGGA 600
| | | | |
Db 659 ----- 658
| | | | |
QY 601 AGGAGCATCCGGTGCCTCGAAGAACATCATCCACTGGAACCTCATCTCGCCTTTCATCTG 660
| | | | |
Db 659 AGGAGCATCCGGTGCCTCGAAGAACATCATCCACTGGAACCTCATCTCGCCTTTCATCTG 718
| | | | |
QY 661 CGCAACGCCCACTGGTGTGTCAGCTAAACATGAGCCCGAGGTCCACGAGCAAC 720
| | | | |
Db 719 CGCAACGCCCACTGGTGTGTCAGCTAAACATGAGCCCGAGGTCCACGAGCAAC 778
| | | | |
QY 721 GTGGGCTGGTGCAAGTGGTGACAGCGCCTCAACACTTCCATGTGACCAACTCTTTC 780
| | | | |
Db 779 GTGGGCTGGTGCAAGTGGTGACAGCGCCTCAACACTTCCATGTGACCAACTCTTTC 838
| | | | |
QY 781 TGGATGTTCCGGCAGGGCTGCTACTGCAACAGCCATCGTGTCTCACTACTCCACTGAC 840
| | | | |
Db 839 TGGATGTTCCGGCAGGGCTGCTACTGCAACAGCCATCGTGTCTCACTACTCCACTGAC 898
| | | | |
QY 841 CGGCTGGCAAAATGGATGTTTCATCTGCAATTTGGCTGGGGTGTGCCCTTCCCATCATTTGTG 900
| | | | |
Db 899 CGGCTGGCAAAATGGATGTTTCATCTGCAATTTGGCTGGGGTGTGCCCTTCCCATCATTTGTG 958
| | | | |
QY 901 GCCTGGGCCAATGGGAGCTGTACTACGACAAATGAGAGTCTGGTTGGCAAAAGCCCT 960
| | | | |
Db 959 GCCTGGGCCAATGGGAGCTGTACTACGACAAATGAGAGTCTGGTTGGCAAAAGCCCT 1018
| | | | |
QY 961 GGGGTGTACACCGACTACATCTACCAGGGCCCCATGATCCTGGTCTCTGTGATCAATTTTC 1020
| | | | |
Db 1019 GGGGTGTACACCGACTACATCTACCAGGGCCCCATGATCCTGGTCTCTGTGATCAATTTTC 1078
| | | | |
QY 1021 ATCTTCCTTTTCAACATGTCGCGATCCTCATGACAAAGTCCGGGATCCACACAGTCT 1080
| | | | |
Db 1079 ATCTTCCTTTTCAACATGTCGCGATCCTCATGACAAAGTCCGGGATCCACACAGTCT 1138
| | | | |
QY 1081 GAGACCAATTCAGTACAGGAGCTGTGAAGCCACTCTGGTGTCTGCGCCCTCCCTGGGC 1140
| | | | |
Db 1139 GAGACCAATTCAGTACAGGAGCTGTGAAGCCACTCTGGTGTCTGCGCCCTCCCTGGGC 1198
| | | | |
QY 1141 ATCACTTACATGCTGTTCTTCGTAATTCGGGGAGGATGAGGTCTCCCGGGTCTCTTC 1200
| | | | |
Db 1199 ATCACTTACATGCTGTTCTTCGTAATTCGGGGAGGATGAGGTCTCCCGGGTCTCTTC 1258
| | | | |
QY 1201 ATCTTCTTCAACTCTTCTCGTAATCTTCAGGGCTTCTTGTGTGTGTCTTACTGT 1260
| | | | |
Db 1259 ATCTTCTTCAACTCTTCTCGTAATCTTCAGGGCTTCTTGTGTGTGTCTTACTGT 1318
| | | | |
QY 1261 TTCTCTCAATAGTGGGTCCGTTCTGTCATCCGGAAGAGTGGCACCGGTGGCAGGCAAG 1320
| | | | |
Db 1319 TTCTCTCAATAGTGGGTCCGTTCTGTCATCCGGAAGAGTGGCACCGGTGGCAGGCAAG 1378
| | | | |
QY 1321 CACTCGATCCGTGCCCGAGTGGCCCGTGGCCATGTCTCATCCCACTCCCAACCCCGTGC 1380
| | | | |

1379 CACTCGATCCGTGCCCGAGTGGCCCGTGCATGTCATCCCACTCCCAACCCCGTGC 1438
| | | | |
QY 1381 AGCTTTTCACAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTTCATGAGCAGCCCC 1440
| | | | |
Db 1439 AGCTTTTCACAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTTCATGAGCAGCCCC 1498
| | | | |
QY 1441 CAAAGAGCTGTGCTGGGGGATGAGCGGCAGGCTCCCTGACCACTGCCTGTGGAGGT 1500
| | | | |
Db 1499 CAAAGAGCTGTGCTGGGGGATGAGCGGCAGGCTCCCTGACCACTGCCTGTGGAGGT 1558
| | | | |
QY 1501 GACTCTGTAGGTCTCATGCCCCACTCCCCCAGGAGCAGCTGGCACTGACAGCTGGGGGG 1560
| | | | |
Db 1559 GACTCTGTAGGTCTCATGCCCCACTCCCCCAGGAGCAGCTGGCACTGACAGCTGGGGGG 1618
| | | | |
QY 1561 CGGCTCTCCCCCTGCGAGCCGTG 1582
| | | | |
Db 1619 CGGCTCTCCCCCTGCGAGCCGTG 1640
| | | | |
RESULT 13
ADO50782
ID ADO50782 standard; cDNA; 2536 BP.
XX
AC ADO50782;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human corticotropin releasing factor receptor 1, CRF1R, cDNA.
XX
KW Human; ss; gene; corticotropin releasing factor receptor; CRF1R; CRF2R;
KW skeletal muscle; muscle atrophy; skeletal muscle dystrophy;
KW skeletal muscle hypertrophy; surgery; bed rest; broken bone;
KW infectious disease; AIDS cachexia.
XX
OS Homo sapiens.
XX
PN US2004101911-A1.
XX
PD 27-MAY-2004.
XX
PF 27-AUG-2003; 2003US-00649852.
XX
PR 06-MAR-2001; 2001US-00799978.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Isfort RJ, Sheldon RJ;
XX
DR WPI; 2004-459890/43.
DR P-PSDB; ADO50783.
XX
PT Identifying compounds for regulating skeletal muscle mass or function, by
FT contacting test compound with vertebrate corticotropin releasing factor2
PT receptors (CRF2R), selecting compounds that bind or activate CRF2R.
XX
PS Disclosure; SEQ ID NO 1; 100pp; English.
XX
CC The invention relates to identifying candidate compounds for regulating
CC skeletal muscle mass or function, comprising contacting a test compound
CC with vertebrate corticotropin releasing factor 2 receptors (CRF 2 R),
CC determining if the compound binds to or activates CRF2R, selecting
CC compounds that bind or activate CRF 2 R, and determining if compound
CC increases muscle mass or function in muscle atrophy model. Also included
CC are identifying candidate therapeutic compounds from a group of one or
CC more candidate compounds which have been previously determined to bind to
CC or activate a vertebrate CRF 2 R (comprising administering the candidate
CC compound to a non-human animal and determining whether the candidate
CC compound regulates skeletal muscle mass or function in the treated
CC animal), increasing skeletal muscle mass or function in a subject in
CC which such an increase is desirable (comprising identifying a subject in
CC which an increase in muscle mass or function is desirable and
CC administering to the subject a safe and effective amount of a CRF 2 R

CC agonist), a purified antibody specific for a CRP2R (where the antibody is
CC a chimaeric or human antibody), and a pharmaceutical composition
CC comprising a safe and effective amount of a CRP2R agonist and carrier.
CC The methods are useful for identifying candidate compounds for regulating
CC skeletal muscle mass or function, for increasing skeletal muscle mass or
CC function (in a subject in which an increase is desirable), for
CC identifying candidate compounds that are potentially useful in the
CC treatment of skeletal muscle dystrophy and for identifying compounds that
CC prolong or augment the agonist-induced activation of CRP2R or of a CRP2R
CC signal transduction pathway. The compound is useful for treating skeletal
CC muscle hypertrophy and for modulating skeletal muscle atrophy induced by
CC e.g. surgery, bed rest, broken bones, infectious disease or AIDS
CC cachexia. The present sequence encodes a corticotropin releasing factor
CC receptor.
XX

SQ Sequence 2536 BP; 478 A; 836 C; 724 G; 498 T; 0 U; 0 Other;

Query Match 88.3%; Score 1396.4; DB 12; Length 2536;

Best Local Similarity 94.4%; Pred. No. 0;

Matches 1494; Conservative 0; Mismatches 1; Indels 87; Gaps 1;

QY 1 CGAGCCGCGAGCCGCGCGCGTTCCTCTGGGATGTCCTGAGGACCCGGGCAATTCAGGAC 60
DB 146 CGAGCCGCGAGCCGCGCGCGTTCCTCTGGGATGTCCTGAGGACCCGGGCAATTCAGGAC 205
QY 61 GGTAGCCGAGCGAGCCGCGAGATGGAGGACCCCGCAGCTCCGTCCTGTCAGGCGCCCTT 120
DB 206 GGTAGCCGAGCGAGCCGCGAGATGGAGGACCCCGCAGCTCCGTCCTGTCAGGCGCCCTT 265
QY 121 CTCTCTCTGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCCAGCTCCGTCCTGTCAGGCGCTG 180
DB 266 CTCTCTCTGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCCAGCTCCGTCCTGTCAGGCGCTG 325
QY 181 TCCCTGCGCAGCAACATCTCAGGACTGCAGTGCAACCATCCGTCGACCTCATTTGGCAAC 240
DB 326 TCCCTGCGCAGCAACATCTCAGGACTGCAGTGCAACCATCCGTCGACCTCATTTGGCAAC 385
QY 241 TGTGCGCCCGCAGCCCTGCGGGCAGCTAGTGTTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 386 TGTGCGCCCGCAGCCCTGCGGGCAGCTAGTGTTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 445
QY 301 GGTGTCGCTACATATACCAACAAATGGCTACCGGAGTGCTTCCGCAATGGCAGCTGG 360
DB 446 GGTGTCGCTACATATACCAACAAATGGCTACCGGAGTGCTTCCGCAATGGCAGCTGG 505
QY 361 GCGCGCCGCTGAATTAATCTCGAGTGCAGAGATCTCAATGAGGAGAGAGAGAGAGAGAGAGAG 420
DB 506 GCGCGCCGCTGAATTAATCTCGAGTGCAGAGATCTCAATGAGGAGAGAGAGAGAGAGAGAGAG 565
QY 421 GTGCACCTACCATGTGCGAGTCAATCAACTACCTGGGCGCACTGTATCTCCCTGCTGGGCC 480
DB 566 GTGCACCTACCATGTGCGAGTCAATCAACTACCTGGGCGCACTGTATCTCCCTGCTGGGCC 625
QY 481 CTCTGCTGCGCTTTGCTCTCTCTCTGCGCTCAGGCGCAGCTGCACCCATTTGGGGTGAC 540
DB 626 CTCTGCTGCGCTTTGCTCTCTCTCTGCGCTC----- 658
QY 541 CAGGACATGGAGCCCTGGAGGTGGGGCTCCATGGAGTGTGGCCCAATTCAGGTTTGA 600
DB 659 ----- 658
QY 601 AGGAGCATCCGGTGCCTGCGAACAATCATCCACTGGAACCTCATCTCCGCTTCATCCTG 660
DB 659 AGGAGCATCCGGTGCCTGCGAACAATCATCCACTGGAACCTCATCTCCGCTTCATCCTG 718
QY 661 CGCAACGCCACCTGGTTGCTGGTCCAGCTAACATGAGCCCGGAGGTCCACAGAGCAAC 720
DB 719 CGCAACGCCACCTGGTTGCTGGTCCAGCTAACATGAGCCCGGAGGTCCACAGAGCAAC 778
QY 721 GTGGGCTGGTGAGGTTGGTGACAGCGCCTTACAACTACTTCCATGTGACCACTTCTTC 780
DB 779 GTGGGCTGGTGAGGTTGGTGACAGCGCCTTACAACTACTTCCATGTGACCACTTCTTC 838

QY 781 TGGATGTTGGCGAGGGCTGCTACCTGCACACAGCCATCGTGTCACTACTCCACTGAC 840
DB 839 TGGATGTTGGCGAGGGCTGCTACCTGCACACAGCCATCGTGTCACTACTCCACTGAC 898
QY 841 CGGCTGCGCAAAATGGATGTTTCATCTGCATTGGCTGGGGTGTGCCCTTCCCCCATCATTTGTG 900
DB 899 CGGCTGCGCAAAATGGATGTTTCATCTGCATTGGCTGGGGTGTGCCCTTCCCCCATCATTTGTG 958
QY 901 GCCTGGGCCCATTTGGGAAGCTGTACTACGACAATGAGAAGTGTGCTGTTTGGCAAAAGCCCT 960
DB 959 GCCTGGGCCCATTTGGGAAGCTGTACTACGACAATGAGAAGTGTGCTGTTTGGCAAAAGCCCT 1018
QY 961 GGGGTGTACACCCGACTACATCTACCGAGGGCCCATGATCTCTGGTCTCTGCTGATCAATTTTC 1020
DB 1019 GGGGTGTACACCCGACTACATCTACCGAGGGCCCATGATCTCTGGTCTCTGCTGATCAATTTTC 1078
QY 1021 ATCTTCTCTTTTCAACATCGTCCGATCCTCATGACCAAGTCCCGGGCATCCACCACGCTCT 1080
DB 1079 ATCTTCTCTTTTCAACATCGTCCGATCCTCATGACCAAGTCCCGGGCATCCACCACGCTCT 1138
QY 1081 GAGACCAATTCAGTACAGGAAGCTGTGAAAGCCACTCTGTGTGTGCTGCTGCCCTCTCTGGGC 1140
DB 1139 GAGACCAATTCAGTACAGGAAGCTGTGAAAGCCACTCTGTGTGTGCTGCTGCCCTCTCTGGGC 1198
QY 1141 ATCACCTACATGCTGTTCTTCTCAATCCCGGGAGGATGAGGTCTCCCGGTCTCTTTC 1200
DB 1199 ATCACCTACATGCTGTTCTTCTCAATCCCGGGAGGATGAGGTCTCCCGGTCTCTTTC 1258
QY 1201 ATCTACTTCAACTCTTCTTCTGGAATCCTTCCAGGGCTTCTTGTGTGCTGTGTTTCTACTGT 1260
DB 1259 ATCTACTTCAACTCTTCTTCTGGAATCCTTCCAGGGCTTCTTGTGTGCTGTGTTTCTACTGT 1318
QY 1261 TTCTCTCAATAGTAGAGTCCGTTCTTGCCATCCGGAAGAGTGGCACCCGGTGGCAGACAAG 1320
DB 1319 TTCTCTCAATAGTAGAGTCCGTTCTTGCCATCCGGAAGAGTGGCACCCGGTGGCAGACAAG 1378
QY 1321 CACTCGATCCGTCGCGAGTGGCCCGTCCATGTCCATCCCACTCCCAACCCCGTGTG 1380
DB 1379 CACTCGATCCGTCGCGAGTGGCCCGTCCATGTCCATCCCACTCCCAACCCCGTGTG 1438
QY 1381 AGCTTTACACAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCTATGGAGCAGCCCC 1440
DB 1439 AGCTTTACACAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCTATGGAGCAGCCCC 1498
QY 1441 CAAAGAGCTGTGGCTGGGGGATGAGCGCCAGGCTCCCTGACCACTCCCTGCTGTGGAGGT 1500
DB 1499 CAAAGAGCTGTGGCTGGGGGATGAGCGCCAGGCTCCCTGACCACTCCCTGCTGTGGAGGT 1558
QY 1501 GACTGTTAGGTCTCATGCCCACTCCCGCAGGAGCAGCTGGCACTGACAGCTGGGGGGG 1560
DB 1559 GACTGTTAGGTCTCATGCCCACTCCCGCAGGAGCAGCTGGCACTGACAGCTGGGGGGG 1618
QY 1561 CCGCTCTCCCGCTGCAGCCGTG 1582
DB 1619 CCGCTCTCCCGCTGCAGCCGTG 1640

RESULT 14

ACA56762

ID ACA56762 standard; cDNA; 1335 BP.

XX

ACA56762;

XX

DT 06-JUN-2003 (first entry)

XX

DE Human signalling pathway polynucleotide probe SEQ ID NO 1360.

XX

KW Human; probe; ss; array element; Parkinson's disease;

KW signalling pathway population; cancer; adenocarcinoma; leukaemia;

KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

XX

OS Homo sapiens.

XX

PN US6500938-B1.
XX 31-DEC-2002.
XX 30-JAN-1998; 98US-00016434.
XX 30-JAN-1998; 98US-00016434.
XX (INCY-) INCYTE GENOMICS INC.
XX Au-Young J, Seilhamer JJ;
XX WPI; 2003-352189/33.
XX
XX Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides.
XX
XX Claim 1; SEQ ID NO 1360; 65pp; English.
XX
XX The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensic and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=06500938B1
XX
XX Sequence 1335 BP; 249 A; 432 G; 350 G; 304 T; 0 U; 0 Other;

Query Match 84.4%; Score 1335; DB 10; Length 1335;
Best Local Similarity 100.0%; Pred. No. 3.5e-313;
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 ATGGGAGGCGACCGCAGCTCCGTCGTCAGGCGCCCTCTCTGCGGCTGMAACCCC 141
DB 1 ATGGGAGGCGACCGCAGCTCCGTCGTCAGGCGCCCTCTCTGCGGCTGMAACCCC 60

QY 142 GTCTCTGCTCCCTCCAGGACCAAGCAGCTGCGAGAGCTGTCCTCTGCGGCGTGAACCTCA 201
DB 61 GTCTCTGCTCCCTCCAGGACCAAGCAGCTGCGAGAGCTGTCCTCTGCGGCGTGAACCTCA 120

QY 202 GGACTGAGTGCAACGCACTCCGTGGAACCTCATTTGGCACTGCTGCGGCCGCGACCCCTGGG 261
DB 121 GGACTGAGTGCAACGCACTCCGTGGAACCTCATTTGGCACTGCTGCGGCCGCGACCCCTGGG 180

QY 262 GGGCAGCTAGTGGTTCGGCCCTGCGCCCTTTCTATGGTTCGCGCTACATATACCACA 321
DB 181 GGGCAGCTAGTGGTTCGGCCCTGCGCCCTTTCTATGGTTCGCGCTACATATACCACA 240

QY 322 AACATAGGCTACCGGGAGTGCCTGGGCAATGGCAGCTGGGCGCGCCGCTGAATTAATCC 381
DB 241 AACATAGGCTACCGGGAGTGCCTGGGCAATGGCAGCTGGGCGCGCCGCTGAATTAATCC 300

QY 382 GAGTGCAGGAGATCTCAATAGAGGAGAAAAAGCAAGGTGCACTACCAATGCGCAGTC 441
DB 301 GAGTGCAGGAGATCTCAATAGAGGAGAAAAAGCAAGGTGCACTACCAATGCGCAGTC 360

QY 442 ATCATCAACTACCTGGGCCACTGTATCTCCCTGGTGGCCCTCTCTGTGGCCCTTTGTCTTC 501
DB 361 ATCATCAACTACCTGGGCCACTGTATCTCCCTGGTGGCCCTCTCTGTGGCCCTTTGTCTTC 420

QY 502 TTTCTGCGGCTCAGGCTCAGGCTGACCCCATTTGGGTTGACAGGAGATGGAGCCCTGGAG 561
DB 421 TTTCTGCGGCTCAGGCTCAGGCTGACCCCATTTGGGTTGACAGGAGATGGAGCCCTGGAG 480

QY 562 GTGGGGGCTCCATGGAGTGGTCCCATTTCAAGTTTGAAGGAGCATCCGCTGCTCCGCA 621
DB 481 GTGGGGGCTCCATGGAGTGGTCCCATTTCAAGTTTGAAGGAGCATCCGCTGCTCCGCA 540

QY 622 AACATCACTACCTGGAACTCATCTCGGCTTTCATCTCTGCGCAACGCCACCTGGTTCTGTG 681
DB 541 AACATCACTACCTGGAACTCATCTCGGCTTTCATCTCTGCGCAACGCCACCTGGTTCTGTG 600

QY 682 GTCCAGCTAACCATAGAGCCCGAGGTCCACAGAGCAACGTGGGCTGTGGAGTTGGTG 741
DB 601 GTCCAGCTAACCATAGAGCCCGAGGTCCACAGAGCAACGTGGGCTGTGGAGTTGGTG 660

QY 742 ACAGCGGCTTACACTTCTTCCATGTGACCAACTTCTTCTGAGATGTTCCGGGAGGCTGC 801
DB 661 ACAGCGGCTTACACTTCTTCCATGTGACCAACTTCTTCTGAGATGTTCCGGGAGGCTGC 720

QY 802 TACCTGCACACAGCCATCGTCTCACTACTCCACTGACCGCTGCGCAAAATGGATGTTTC 861
DB 721 TACCTGCACACAGCCATCGTCTCACTACTCCACTGACCGCTGCGCAAAATGGATGTTTC 780

QY 862 ATCTGCATTTGGTGGGTGTGCGCTTCCCATCATTTGTGGCTGTGGCCCATTTGGGAAGCTG 921
DB 781 ATCTGCATTTGGTGGGTGTGCGCTTCCCATCATTTGTGGCTGTGGCCCATTTGGGAAGCTG 840

QY 922 TACTAGCAATGAGAGTGTGGTTTGGCAAAAGCCCTGGGGTGTACACCGACTACATC 981
DB 841 TACTAGCAATGAGAGTGTGGTTTGGCAAAAGCCCTGGGGTGTACACCGACTACATC 900

QY 982 TACCAGGGCCCATGATCTGCTGCTGCTGATCAATTTCTCTTTTCAACATCTGTC 1041
DB 901 TACCAGGGCCCATGATCTGCTGCTGCTGATCAATTTCTCTTTTCAACATCTGTC 960

QY 1042 CGCATCTCATGACCAAGCTCCGGGCAATCCACGCTCTGAGACCAATTCAGTACAGGAAG 1101
DB 961 CGCATCTCATGACCAAGCTCCGGGCAATCCACGCTCTGAGACCAATTCAGTACAGGAAG 1020

QY 1102 GCTGTGAAGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1161
DB 1021 GCTGTGAAGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080

QY 1162 GTCAATCCCGGGAGGATGAGGTCTCCGGGCTGCTTCTCATCTTCACTTCACTTCTTCTG 1221
DB 1081 GTCAATCCCGGGAGGATGAGGTCTCCGGGCTGCTTCTCATCTTCACTTCTTCTTCTTCT 1140

QY 1222 GAATCTCTCAGGGCTTTTGT 1281
DB 1141 GAATCTCTCAGGGCTTTTGT 1200

QY 1282 TCTGCCATCCGAGAGGTGGACCGGTGGCAGGACCAAGCACTCGATCCGTCGCCGAGTG 1341
DB 1201 TCTGCCATCCGAGAGGTGGACCGGTGGCAGGACCAAGCACTCGATCCGTCGCCGAGTG 1260

QY 1342 GCGCGTGCCATGTCCATCCCACTCCCACTCCCACTCCCACTCCCACTCCCACTCCCACTCCCA 1401
DB 1261 GCGCGTGCCATGTCCATCCCACTCCCACTCCCACTCCCACTCCCACTCCCACTCCCACTCC 1320

QY 1402 TCCACAGCAGTCTGA 1416
DB 1321 TCCACAGCAGTCTGA 1335

RESULT 15
AD156558
ID AD156558 standard; DNA; 1335 BP.
XX

AC ADI56558;
XX 22-APR-2004 (first entry)
XX Human polynucleotide probe #1360.
XX Human; probe; ss; receptor-like polypeptide; transducing polypeptide;
KW effector-like polypeptide; cancer; immunopathology; neuropathology;
KW drug development; toxicology; carcinogenicity;
KW signalling pathway polypeptide; adrenal gland;
KW bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;
KW diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;
KW dementia; amnesia; epilepsy; Alzheimer's disease; depression.
XX Homo sapiens.
XX US2004010136-A1.
XX 15-JAN-2004.
XX 26-NOV-2002; 2002US-00305720.
XX 30-JAN-1998; 98US-00016434.
XX (INCY-) INCYTE GENOMICS INC.
XX Au-Young J, Seilhamer JJ;
XX WPI; 2004-090520/09.
XX New composition comprising polynucleotide probes, useful as array
PT elements in a microarray for monitoring the expression of target
PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
PT fragments.
XX Claim 6; SEQ ID NO 1360; 73pp; English.
XX The invention relates to a composition of polynucleotide probes
CC comprising first polynucleotide probes comprising at least a portion of a
CC gene encoding a receptor-like polypeptide, second polynucleotide probes
CC comprising at least a portion of a gene encoding a transducing
CC polypeptide and third polynucleotide probes comprising at least a portion
CC of a gene encoding an effector-like polypeptide. The probes of the
CC composition are useful as array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray is useful in the
CC diagnosis and treatment of cancer, an immunopathology or a
CC neuropathology. It can also be used for drug discovery and development.
CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.
CC Microarrays can also be used for monitoring the progression of diseases
CC that may be associated with the altered expression of signalling pathway
CC polypeptides. The composition can also be used to purify a subpopulation
CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile
CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of
CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,
CC epilepsy, Alzheimer's disease or depression. This sequence represents a
CC human polynucleotide probe of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX Sequence 1335 BP; 249 A; 432 C; 350 G; 304 T; 0 U; 0 Other;
Query Match 84.4%; Score 1335; DB 12; Length 1335;
Best Local Similarity 100.0%; Pred. No. 3.5e-313;
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 82 ATGGAGGGGACCCGAGCTCCGTCCTCGTCAAGGCCCTTCTCTTCCTTCGCGGCTGAACCCC 141
DB 1 ATGGAGGGGACCCGAGCTCCGTCCTCGTCAAGGCCCTTCTCTTCCTTCGCGGCTGAACCCC 60
QY 142 GTCTCTGCTCCCTCCAGGACCAAGCACTGCGAGAGCCTGTCTCTGCGCCAGCAATCTCA 201

61 GTCTCTGCTCCCTCCAGGACCAAGCACTGCGAGAGCCTGTCTCTGCGCCAGCAATCTCA 120
QY 202 GGATCGAGTGCAACGCATCCGTTGGACCTCATTTGGCACTGTGTGGCCCGCCGCTGGG 261
DB 121 GGATCGAGTGCAACGCATCCGTTGGACCTCATTTGGCACTGTGTGGCCCGCCGCTGGG 180
QY 262 GGGCAGCTAGTGGTTGGCCCTGCTGCTTTTCTATGTTGTTCTGCTGCTACATACCA 321
DB 181 GGGCAGCTAGTGGTTGGCCCTGCTGCTTTTCTATGTTGTTCTGCTGCTACATACCA 240
QY 322 AACAAATGGGTACCGGAGTGCTGGGCAATGGCAGCTGGGCCCCCGCGCTGAATTA 381
DB 241 AACAAATGGGTACCGGAGTGCTGGGCAATGGCAGCTGGGCCCCCGCGCTGAATTA 300
QY 382 GAGTGCAGGAGATCCTCAATGAGGAGAAAGCAAGAGTGCACTACCAATGTGCGAGTC 441
DB 301 GAGTGCAGGAGATCCTCAATGAGGAGAAAGCAAGAGTGCACTACCAATGTGCGAGTC 360
QY 442 ATCATCAACTACCTGGGCCACTGTATCTCCCTGGTGGCCCTCTGCTGGGCTTTGTCCTC 501
DB 361 ATCATCAACTACCTGGGCCACTGTATCTCCCTGGTGGCCCTCTGCTGGGCTTTGTCCTC 420
QY 502 TTTCTCGGCTCAGGCCAGGCTGACCCATTTGGGGTGACCCAGGAGATGAGGCCCTGGAG 561
DB 421 TTTCTCGGCTCAGGCCAGGCTGACCCATTTGGGGTGACCCAGGAGATGAGGCCCTGGAG 480
QY 562 GTGGGGCTCCATGGAGTGGTGCCTCCATTTCAAGTTGCAAGGAGCATTCGGTGCCTGCGA 621
DB 481 GTGGGGCTCCATGGAGTGGTGCCTCCATTTCAAGTTGCAAGGAGCATTCGGTGCCTGCGA 540
QY 622 AACATCATCACTGGAACCTCATCTCGGCTTCACTCTGCGGCAACGCCACCTGTTGCTG 681
DB 541 AACATCATCACTGGAACCTCATCTCGGCTTCACTCTGCGGCAACGCCACCTGTTGCTG 600
QY 682 GTCCAGCTAACCAATGAGCCCGAGGCTCACAGAGCAAGTGGGCTGGTGCAGTGGTGG 741
DB 601 GTCCAGCTAACCAATGAGCCCGAGGCTCACAGAGCAAGTGGGCTGGTGCAGTGGTGG 660
QY 742 ACAGCCGCTTACAACTACTTCCATGTGACCAACTTCTTCTGATGTTTGGCGAGGGCTGC 801
DB 661 ACAGCCGCTTACAACTACTTCCATGTGACCAACTTCTTCTGATGTTTGGCGAGGGCTGC 720
QY 802 TACTGCAACAGCCATCGTGTCTCACTACTCACTGACCGGCTGGCGAAATGATGTTTC 861
DB 721 TACTGCAACAGCCATCGTGTCTCACTACTCACTGACCGGCTGGCGAAATGATGTTTC 780
QY 862 ATCTGCAATGGCTGGGGTGGCCCTTCCCATCATTTGGCCCTGGGCAATTGGGAAGCTG 921
DB 781 ATCTGCAATGGCTGGGGTGGCCCTTCCCATCATTTGGCCCTGGGCAATTGGGAAGCTG 840
QY 922 TACTACGACAATGAGAAGTGTCTGTTTGGCAAGGCTGGGGTGTACACCGACTACATC 981
DB 841 TACTACGACAATGAGAAGTGTCTGTTTGGCAAGGCTGGGGTGTACACCGACTACATC 900
QY 982 TACAGGGGCCCCATGATCTGTCCTGCTGATCAATTTCAATCTCTTTTCAACATCGTC 1041
DB 901 TACAGGGGCCCCATGATCTGTCCTGCTGATCAATTTCAATCTCTTTTCAACATCGTC 960
QY 1042 CGCATCTCATGACCAAGCTCCGGGCACTCCACCACTCTGAGACCACTTCACTAGTACAGG 1101
DB 961 CGCATCTCATGACCAAGCTCCGGGCACTCCACCACTCTGAGACCACTTCACTAGTACAGG 1020
QY 1102 GCTGTGAAGGCCACTCTGTTGCTGCTGCCCTCTCTGGGCACTACCTACATGCTGTTCTTC 1161
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Search completed: March 17, 2006, 10:52:33
 Job time : 1006 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 17, 2006, 09:54:53 ; Search time 8122 Seconds
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Title: US-10-649-193-14
Perfect score: 1582
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: gb_ba.*
- 2: gb_in.*
- 3: gb_env.*
- 4: gb_cm.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sts.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_vi.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1582	100.0	1582	6 AR211447	AR211447 Sequence
2	1582	100.0	1582	6 AR255739	AR255739 Sequence
3	1582	100.0	1582	6 AR266802	AR266802 Sequence
4	1582	100.0	1582	6 AR412107	AR412107 Sequence
5	1398	88.4	1495	6 AR211440	AR211440 Sequence
6	1398	88.4	1495	6 AR255732	AR255732 Sequence
7	1398	88.4	1495	6 AR266795	AR266795 Sequence
8	1398	88.4	1495	6 AR412100	AR412100 Sequence
9	1396.4	88.3	2536	6 AR442670	AR442670 Sequence
10	1396.4	88.3	2536	8 HSCRPA	X72304 H. sapiens m
11	1335	84.4	1335	6 AR270797	AR270797 Sequence
12	1335	84.4	1335	8 HUMCRFRB	L23333 Human corti
13	1283.8	81.2	2374	8 AB078141	AB078141 Macaca mu
14	1283	81.1	1380	6 I92584	I92584 Sequence 1
15	1188	75.1	1285	6 AR442671	AR442671 Sequence
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17	1154.2	73.0	10042	6 AX469664	AX469664 Sequence
18	1151	72.8	1248	6 AX469662	AX469662 Sequence

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24	1149	72.6	1248	11 BT019510	BT019510 Synthetic
25	1148	72.6	1245	6 E11431	E11431 cDNA encodi
26	1060.6	67.0	1454	4 TBR422241	TA422241 Tupaia be
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LOCUS AR211447 1582 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 14 from patent US 6399315.
ACCESSION AR211447
VERSION AR211447.1 GI:21514771
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1582)
AUTHORS Perrin,M.H., Chen,R., Lewis,K.A., Vale,W.W. Jr., Donaldson,C.J. and Sawchenko,P.
TITLE Screening assays using cloned CRF receptors
JOURNAL Patent: US 6399315-A 14 04-JUN-2002;
FEATURES Location/Qualifiers
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Qy	181	TCCTCGGCGAGCAATCTCAGGACTGCAGTGCAGCAAGCATCCGTGGACCTCATTTGGCACC	240	
Db	181	TCCTCGGCGAGCAATCTCAGGACTGCAGTGCAGCAAGCATCCGTGGACCTCATTTGGCACC	240	

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RESULT 3
LOCUS AR266802 1582 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 14 from patent US 6495343.
ACCESSION AR266802
VERSION AR266802.1 GI:29696126
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1582)
AUTHORS Perrin,M.H., Chen,R., Lewis,K.A., Vale,W.W. Jr., Donaldson,C.J. and Sawchenko,P.
TITLE Cloning and recombinant production of CRF receptor(s)
JOURNAL Patent: US 6495343-A 14 17-DEC-2002;
The Salk Institute for Biological Studies; La Jolla, CA
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LOCUS AR412107 1582 bp DNA linear PAT 18-DEC-2003
 DEFINITION Sequence 14 from patent US 6638905.
 ACCESSION AR412107
 VERSION AR412107.1 GI:40164666
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1582)
 AUTHORS Perrin,M.H., Chen,R., Lewis,K.A., Vale,W.W. Jr., Donaldson,C.J. and Sawchenko,P.
 TITLE Cloning and recombinant production of CFR receptor(s)
 JOURNAL Patent: US 6638905-A 14 28-OCT-2003;
 The Salk Institute for Biological Studies; La Jolla, CA
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 Best Local Similarity 100.0%; Pred. No. 2.5e-287;
 Matches 1582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 601 AGAGCATCCGCTGCTGCGAAACATCATCTGGAACCTCATCTCCGCTTCATCTCTG 660
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1474 CCGCTCTCCCGCTGCAGCCGTG 1495

RESULT 8
AR412100
LOCUS AR412100 1495 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6638905.
ACCESSION AR412100
VERSION AR412100.1 GI:40164659
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1495)
AUTHORS Perrin,M.H., Chen,R., Lewis,K.A., Vale,W.W. Jr., Donaldson,C.J. and Sawchenko,P.
TITLE Cloning and recombinant production of CFR receptor(s)
JOURNAL Patent: US 6638905-A 1 28-OCT-2003;
The Salk Institute for Biological Studies; La Jolla, CA
FEATURES
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Query Match 88.4%; Score 1398; DB 6; Length 1495;
Best Local Similarity 94.5%; Pred. No. 1e-252;
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574 CGCAACGCCACCTGGTTCGAGTAAACATGAGCCCCCGAGGTTCACACGAGACAAC 633
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Db 1414 GACCTGTAGGTCTCATGCCCATCCGCCAGGAGCAGCTGGCACTGACAGCCCTGGGGGG 1473
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RESULT 9
LOCUS AR442670 2536 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1 from patent US 6670140.
ACCESSION AR442670
VERSION AR442670.1 GI:42669939
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2536)
AUTHORS Isfort, R.J. and Sheldon, R.J.
TITLE Methods for identifying compounds for regulating muscle mass or function using corticotropin releasing factor receptors
JOURNAL Patent: US 6670140-A 1 30-DEC-2003;
The Procter & Gamble Company; Cincinnati, OH
FEATURES
source Location/Qualifiers
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ORIGIN

Query Match 88.3%; Score 1396.4; DB 6; Length 2536;
Best Local Similarity 94.4%; Pred. No. 1.9e-252;
Matches 1494; Conservative 0; Mismatches 1; Indels 87; Gaps 1;

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Db      1619  CCGCTCTCCCTCCGCGAGCGCTG 1640
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LOCUS   HSCRFA                2536 bp      mRNA      linear      PRI 17-FEB-1997
DEFINITION H.sapiens mRNA for corticotrophin releasing factor receptor.
ACCESSION X72304
VERSION   X72304.1  GI:436118
KEYWORDS corticotropin releasing factor receptor.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
           Eukaryota; Metazoa; Euarchontoglires; Primates; Catarrhini;
           Hominiidae; Homo.
REFERENCE
AUTHORS  Vita,N., Laurent,P., Lefort,S., Chalon,P., Lelias,J.M., Kaghad,M.,
           Le Fur,G., Caput,D. and Ferrara,P.
TITLE     Primary structure and functional expression of mouse pituitary and
           human brain corticotrophin releasing factor receptors
JOURNAL   FEBS Lett. 335 (1), 1-5 (1993)
PUBMED    8243652
REFERENCE
AUTHORS  Odenakker,G., Fiten,P., Nys,G., Froyen,G., Van Roy,N.,
           Speleman,P., Laureys,G. and Van Damme,J.
TITLE     The human MCP-3 gene (SCYA7): cloning, sequence analysis, and
           assignment to the C-C chemokine gene cluster on chromosome
           17q11.2-q12
JOURNAL   Genomics 21 (2), 403-408 (1994)
PUBMED    7916328
REFERENCE
AUTHORS  Caput,D.
TITLE     Direct Submission
JOURNAL   INNOPOLE - BP 137- Voie N 1, 31676, Labège Cedex, FRANCE
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Query Match      88.3%; Score 1396.4; DB 8; Length 2536;
Best Local Similarity 94.4%; Pred. No. 1.9e-252;
Matches 1494; Conservative 0; Mismatches 1; Indels 87; Gaps 1;
QY      1  CGAGCCGCGAGCCGCGCGGTCCTCTCGGATGTCCTGAGGACCGGGGCATTTCAGGAC 60
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Db	1379	CACCTCGATCCGTTGCCCGCAGATGGCCGTCGATGCCATGCCCACTCCCAACCCCGTGTCT	1438
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Db	1559	GACCTGTTAGGTCTCATGCCACATCCCCACAGGAGCAGCTGGCACTGACGCTGGGGGGG	1618
Qy	1561	CCGCTCTCCCCCTGCAGCCGCTG 1582	
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DEFINITION	Sequence 1360 from patent US 6500938.		
ACCESSION	AR270797		
VERSION	AR270797.1 GI:29702031		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1335)		
AUTHORS	Au-Young,J. and Sellhammer,J.J.		
TITLE	Composition for the detection of signaling pathway gene expression		
JOURNAL	Patent: US 6500938-A 1360 31-DEC-2002;		
	Incyte Genomics, Inc.; Palo Alto, CA;		
	WOX;		
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Best Local Similarity 100.0%; Pred.No. 7.5e-241;			
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Qy	262	GGGAGCTAGTGGTTGGGCCCTGCCCTGCTTTTCTATGGTGTCCGCTACATACCACA	321
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RESULT 12
LOCUS HUMCRFRB 1335 bp mRNA linear PRI 22-OCT-1993
DEFINITION Human corticotropin releasing factor receptor mRNA, complete cds.
ACCESSION L23333
VERSION L23333.1 GI:408691
KEYWORDS corticotropin releasing factor receptor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1335)
AUTHORS Chen,R., Lewis,K.A., Perrin,M.H. and Vale,W.W.
TITLE Expression cloning of a human corticotropin-releasing-factor
receptor
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90 (19), 8967-8971 (1993)
PUBMED 7692441
COMMENT Original source text: Homo sapiens Human Corticotrope Adenoma cDNA
to mRNA.
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AB078141
LOCUS AB078141 2374 bp mRNA linear PRI 02-DEC-2003
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DEFINITION Macaca mulatta CRF1 mRNA for corticotropin releasing factor receptor type 1, complete cds.
ACCESSION AB078141
VERSION AB078141.1 GI:38602677
KEYWORDS
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE
AUTHORS Oshida, Y., Ikeda, Y., Chaki, S. and Okuyama, S.
TITLE Monkey corticotropin releasing factor1 receptor: cDNA cloning and pharmacological characterization
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2374)
AUTHORS Oshida, Y., Ikeda, Y., Chaki, S. and Okuyama, S.
TITLE Direct Submission
JOURNAL Submitted (16-JAN-2002) Yuichi Oshida, Medicinal Research Laboratories, Taisho Pharmaceutical Co., Ltd., Medicinal Pharmacology Laboratory; 1-403, Yoshino-cho, Saitama 330-8530, Japan (E-mail: y.oshida@po.rd.taisho.co.jp, Tel: 81-48-669-3028, Fax: 81-48-652-7254)
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VERSION 192584.1 GI:3937054
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REFERENCE 1 (bases 1 to 1380)
AUTHORS Perrin,M.H., Chen,R., Lewis,K.A., Vale,W.W. Jr. and Donaldson,C.J.
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JOURNAL Patent: US 5728545-A 1 17-MAR-1998;
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ACCESSION AR442671
VERSION AR442671.1 GI:42669940
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1285)
AUTHORS Iefort,R.J. and Sheldon,R.J.

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4	822.6	52.0	1248	10	AY414329	AY414329 Mus muscu
5	643.8	40.7	779	6	CF147820	CF147820 AGENCOURT
6	515.2	32.6	581	8	DN396007	DN396007 LTB3935-0
7	514.4	32.5	727	8	DR002290	DR002290 TCI10860
8	491.2	31.0	1148	3	BM925912	BM925912 AGENCOURT
9	469.4	29.7	1176	10	AY406515	AY406515 Homo sapi
10	469.2	29.7	875	8	CX955987	CX955987 JGI_CAA08
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QY 781 TGGATGTTCCGCGAGGCGCTCTACCTGCACACAGCCCATCGTGTCTCACTCTCCACTGAC 840
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QY 841 CGGCTGCGCAATGGATGTTTCATCTGCAATTTGGCTGGGGGTGTGCCCTTCCCATCATTTGTG 900

DB 826 CGGCTGCGCAATGGATGTTTCATCTGCTGCTGGGTGTGCCCTTCCCATCATTTGTG 885

QY 901 GCCTGGGCGCATTTGGGAAGCTGTACTAGCAAAATGAGAAGTGTGTTGGCAAAAGCCCT 960
DB 886 GCCTGGGCGCATTTGGGAAGCTGTACTAGCAAAATGAGAAGTGTGTTGGCAAAAGCCCT 945

QY 961 GGGGTGTACACCGACTACATCTACAGGGGCCCATGATCTGCTCTGCTGATCAATTTTC 1020
DB 946 GGGGTGTACACCGACTACATCTACAGGGGCCCATGATCTGCTCTGCTGATCAATTTTC 1005

QY 1021 ATCTTCTTTTCAACATGTCGTCGATCTCTATGACCAAGCTCCGGGATCCACAGCTCT 1080
DB 1006 ATCTTCTTTTCAACATGTCGTCGATCTCTATGACCAAGCTCCGGGATCCACAGCTCT 1065

QY 1081 GAGACCATTCAGTACAGGAGGCTGTGAAGCACTCTGGTGTGCTGCCCTCTCTGGGC 1140
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DB 1126 ATCACCTACATGCTGTTCTTCTGTCATCCCGGGAGATGAGGTCTCCGGGTCTCTTC 1185

QY 1201 ATCTACTTCAACTCTTCTCTGGAATCTTCCAGGGCTTCTTTGTGTGTGTTCTACTGT 1260
DB 1186 ATCTACTTCAACTCTTCTCTGGAATCTTCCAGGGCTTCTTTGTGTGTGTTCTACTGT 1245

QY 1261 TTCTCTCAATAGTGGCTCGTTCCTGTCATCCGGAAGAGGTGGCAGCGGTGGAGGCAAG 1320
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QY 1321 CACTCCATCCGTCGCCGAGTGGCCGCTGTCATGTCATCCACCTCCCAACCCGCTGTC 1380
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DB 1366 AGCTTTTCAAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTGATGGAGAGCCCC 1425

QY 1441 CAAAGAGCTGTGGCTGGGGGATGAGCGCCAGGCTCCCTGACCACTGCTGCTGGAGGT 1500
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QY 1501 GACTGTGTAGTCTCATGCCCCACTCCCGCAGGAGCAGCTGGGCACTGACAGCTTGGGGGGG 1560
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QY 1561 CGGCTCTCCCGCTGCGAGCGGTG 1582
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RESULT 2

AY414327
LOCUS Homo sapiens CRHR1 gene, VIRTUAL TRANSCRIPT, partial sequence, 1248 bp DNA linear GSS 17-DEC-2003
DEFINITION genomic survey sequence.

ACCESSION AY414327

VERSION AY414327.1

KEYWORDS GI:39770289

SOURCE GSS.

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 1248)

REFERENCE

AUTHORS

Todd, M.A., Tanenbaum, D.M., Givello, D.R., Lu, F., Murphy, B.,

Perrier, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

14671302
2 (bases 1 to 1248)
REFERENCE
AUTHORS
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source
1..1248
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/gene="CRHR1"
/locus_tag="HCM5187"
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Query Match 61.5%; Score 973; DB 10; Length 1248;
Best Local Similarity 80.1%; Pred. No. 4.4e-230;
Matches 1070; Conservative 0; Mismatches 178; Indels 87; Gaps 1;
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1 ATGGAGGGGACCGCAGCTCCGTCTGTCAGAGCCCTTCTCTTCTGGGGCTGAACCCC 60
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61 GTCTCTGCTCCCTCCAGGACACGACTGCGAGAGCCCTGCTCCCTGGCCAGCAATCTCA 120
202 GGACTGCACTGCAACGCACTCCGTCGACCTCAITGGCACTGCTGGCCCGCAGCCCTGGC 261
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262 GGGCAGCTAGTGTTCGGCCCTGCTCCCTGCTCTTTCTATGGTTCGCTACATACACA 321
181 GGGCAGCTAGTGTTCGGCCCTGCTCCCTGCTCTTTCTATGGTTCGCTACATACACA 240
322 AACATGGCTACCGGAGTGCCTGGCCATGAGCAGCTGGCCCGCCGCTGAATCTCTCC 381
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421 TTTCTGGGCTC----- 432
562 GTGGGGCTCCATGAGTGGTGGCCCATTTTCAGGTTTGAAGGAGCATCCGGTCTCGCA 621
433 -----AGGAGCATCCGGTCTCGCA 453
622 AACATCATCACTGGAACTCATCTCGCCCTTCACTCTGGCCAGCAACGCACTGGTTCGTG 681
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QY 862 ATCTGCAATTGGCTGGGGTGTGCCCTTCCCATCATTTGTGGCCTGGGCAATGGGAAGCTG 921
Db 694 ATCTGCAATTGGCTGGGGTGTGCCCTTCCCATCATTTGTGGCCTGGGCAATGGGAAGCTG 753
QY 922 TACTAGCAATGAGAAGTGTGGTTTGGCAAGAGCTGGGGTGTACACCGACTACATC 981
Db 754 TACTAGCAATGAGAAGTGTGGTTTGGCAAGAGCTGGGGTGTACACCGACTACATC 813
QY 982 TACCAGGGCCCCATGATCCTGTCTGTCGATCAATTTTCTCTTTTCAACATCGTC 1041
Db 814 TACCAGGGCCCCATGATCCTGTCTGTCGATCAATTTTCTCTTTTCAACATCGTC 873
QY 1042 CGCATCTCATGACCAAGCTCCGGGCATCCACACGCTGAGACCAATTCAGTACAGGAAG 1101
Db 874 CGCATCTCATGACCAAGCTCCGGGCATCCACACGCTGAGACCAATTCAGTACAGNNN 933
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QY 1162 GTCAATCCCGGGGAGGATGAGGTCTCCCGGTCGTCTTCTACTTCAACTCTCTCTG 1221
Db 994 NNN 1053
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QY 1282 TCTGCCATCCGGAAGAGTGGCAACCGGTGGCAGGACAGCACTCGATCCCTGCCGAGTG 1341
Db 1114 TCTGCCATCCGGAAGAGTGGCAACCGGTGGCAGGACAGCACTCGATCCCTGCCGAGTG 1173
QY 1342 GCCCGTGCCATGTCATCCCATCCCATCCCAACCCGCTGTCAGCTTTTCAACATCAAGCAG 1401
Db 1174 GCCCGTGCCATGTCATCCCATCCCATCCCAACCCGCTGTCAGCTTTTCAACATCAAGCAG 1233
QY 1402 TCCACAGCAGTCTGA 1416
Db 1234 TCCACAGCAGTCTGA 1248
AY414328 1248 bp DNA linear GSS 17-DEC-2003
Pan troglodytes CHRR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
AY414328
AY414328.1 GI:39770290
GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Pan.
1 (bases 1 to 1248)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 1248)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source Location/Qualifiers

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/mol_type="genomic DNA"

/db_xref="taxon:9598"

<1..>1248

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/locus_tag="HMS187"

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Best Local Similarity 79.68; Pred. No. 9.4e-228;

Matches 1063; Conservative 0; Mismatches 185; Indels 87; Gaps 1;

QY 82 ATGGAGGGGACCGCAGCTCCGTCTCGTCAAGGCCCTTCTCTCTCTGCGGCTGAACCCC 141

DB 1 ATGGAGGGGACCGCAGCTCCGTCTCGTCAAGGCCCTTCTCTCTCTGCGGCTGAACCCC 60

QY 142 GTCTCTGCTCCCTCAGGACCAAGCTGCGAGAGCTGTCCTCTGCGGCTGAACCTCA 201

DB 61 GTCTCTGCTCCCTCAGGACCAAGCTGCGAGAGCTGTCCTCTGCGGCTGAACCTCA 120

QY 202 GGACTGCGTGAACGATCCGTGGACCTCATTTGGCACCTGCTGGCCCGCGACCTGGG 261

DB 121 GGACTGCGTGAACGATCCGTGGACCTCATTTGGCACCTGCTGGCCCGCGACCTGGG 180

QY 262 GGGCAGCTAGTGGTTCGGCCCTGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 321

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QY 562 GTGGGGGCTCCATGAGTGGTGCCCAATTCAGGTTTCGAGGAGGAGGAGGAGGAGGAGG 621

DB 433 -----AGGAGATCCGGTGCCTGCGGA 453

QY 622 AACATCATCACTGGAACCTCATCTCGCCCTTCATCTCTGCGCAACGCACTGGTTCGTT 681

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QY 682 GTCCAGTAAACATAGAGCCCGAGGTCACACAGAGCAACGTGGGCTGGTGCAGGTTGGTG 741

DB 514 GTCCAGTAAACATAGAGCCCGAGGTCACACAGAGCAACGTGGGCTGGTGCAGGTTGGTG 573

QY 742 ACAGCCGCTTACAACTATCTTCATGTGACCACTTCTCTCTGATGTTTCGCGAGGAGGCTG 801

DB 574 ACAGCCGCTTACAACTATCTTCATGTGACCACTTCTCTCTGATGTTTCGCGAGGAGGCTG 633

QY 802 TACCTGCACACAGCCATCTGCTCACCCTACTCCACTGACCGGCTGGCGCAATGGATGTTTC 861

DB 634 TACCTGCACACAGCCATCTGCTCACCCTACTCCACTGACCGGCTGGCGCAATGGATGTTTC 693

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DB 694 ATCTGCAATTGGCTGGGCTGGCCCTTCCCATCATTTGTCCTGGGCAATGGGAGGCTG 753

QY 922 TACTACGACATGAGAGTGGTGGTTTGGCAAAAGCCCTGGGGGTGTACACCGACTACATC 981

DB 754 TACTACGACATGAGAGTGGTGGTTTGGCAAAAGCCCTGGGGGTGTACACCGACTACATC 813

QY 982 TACCAGGGCCCCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1041

DB 814 TACCAGGGCCCCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 873

QY 1042 CGCATCTCATGACCAAGCTCCGGGATCCACCAAGCTGAGACCACTTCACTGACAGGAAG 1101

DB 874 CGCATCTCATGACCAAGCTCCGGGATCCACCAAGCTGAGACCACTTCACTGACAGNNN 933

QY 1102 GCTGTGAAAGCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1161

DB 934 NNN 993

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DB 994 NNN 1053

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DB 1234 TCCACAGCAGTCTGA 1248

RESULT 4

AY1414329

LOCUS

DEFINITION Mus musculus CRHR1 gene, VIRTUAL TRANSCRIPT, partial sequence.

ACCESSION AY1414329

VERSION AY1414329.1 GI:39770291

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBLISHED 14671302

REFERENCE 2 (bases 1 to 1248)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source

1.1248

/organism="Mus musculus"

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Db	874	CGCATCCTCATGACCAAACTCCGAGCATCCACCACATCTGAGACTATTTCAGTACAGNNNN	933
Qy	1102	GCTGTGAAGCCACTCTGGTGTGCTGCTGCCCTCTCGGCATCACCTACATGCTGTTCTTC	1161
Db	934	NN	993
Qy	1162	GTCAATCCCGGGGAGGATGAGGTCTCCGGGTGCTCTTCATCTACTTCAACTCCTTCTCTG	1221
Db	994	NN	1053
Qy	1222	GAATCCTTCAGGGCTTCTTTGTGCTGTGTTCTACTGTTTCTCAATAGTAGGTCCTG	1281
Db	1054	NN	1113
Qy	1282	TCGTGCCATCGGAAGAGGTGGCACCGGTGGCAGCAGCAAGCACCTCGATCCGTCGCCGAGTG	1341
Db	1114	TCGTGCCATCGGAAGAGGTGGCGGGATGGCAGCAGCAAGCACCTCCATCAGAGCCCGAGTG	1173
Qy	1342	GCCCGGTGCCATGTCCCATCCCCACCTCCCAACCCGCTGTCAGCTTTTTCACAGCATCAAGCAG	1401
Db	1174	GCCCGGCCATGTCCATCCCCACTCCCCACCAGCAGTCAAGTCTCCACAGCATCAAGCAG	1233
Qy	1402	TCCACAGCAGTGTGA	1416
Db	1234	TCCACAGCAGTGTGA	1248

RESULT 5

CF147820

LOCUS

DEFINITION

AGENCOURT 14740211 NIH MGC 145 Homo sapiens cDNA clone

IMAGE:6971902 5', mRNA sequence.

CF147820

CF147820.1 GI:33244088

EST.

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 779)

NIH-MGC <http://mgc.nci.nih.gov/>.

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

UNPUBLISHED (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: GPCR Consortium

cDNA Library Preparation: GPCR Consortium

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: IRB102 row: b column: 09

High quality sequence start: 8

High quality sequence stop: 738.

FEATURES

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Site 230: varies by clone; Site 231: varies by clone; Site 232: varies by clone; Site 233: varies by clone; Site 234: varies by clone; Site 235: varies by clone; Site 236: varies by clone; Site 237: varies by clone; Site 238: varies by clone; Site 239: varies by clone; Site 240: varies by clone; Site 241: varies by clone; Site 242: varies by clone; Site 243: varies by clone; Site 244: varies by clone; Site 245: varies by clone; Site 246: varies by clone; Site 247: varies by clone; Site 248: varies by clone; Site 249: varies by clone; Site 250: varies by clone; Site 251: varies by clone; Site 252: varies by clone; Site 253: varies by clone; Site 254: varies by clone;

varies by clone; ORFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites for Y3, Y4 and include the following: 5'-EcoRV-XmnI/XhoI-3', 5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clone represents, please visit our anonymous ftp site at http://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat. A Note: this is a NIH MGCC Library."

ORIGIN

Query Match	40.7%;	Score 643.8;	DB 6;	Length 779;
Best Local Similarity	89.2%;	Pred. No. 1.9e-148;		
Matches 742;	Conservative 0;	Mismatches 3;	Indels 87;	Gaps 1;
Qy	82	ATGGGAGGACCGCAGCTCCGCTCGTCAAGGCCCTTCTCTCTGGGGCTGAACCCC	141	
Db	35	ATGGGAGGACCGCGAGCTCCGCTCGTCAAGGCCCTTCTCTCTGGGGCTGAACCCC	94	
Qy	142	GTCTCTGCCTCCCTCCAGGACACGACTCGGAGAGCCTGTCCCTGGCGACCAATCTCA	201	
Db	95	GTCTCTGCCTCCCTCCAGGACACGACTCGGAGAGCCTGTCCCTGGCGACCAATCTCA	154	
Qy	202	GGACTGCAGTGCACGCAATCCGTTGGACCTCATTTGGCACCTGCTGGCCCCCGACGCTTGG	261	
Db	155	GGACTGCAGTGCACGCAATCCGTTGGACCTCATTTGGCACCTGCTGGCCCCCGACGCTTGG	214	
Qy	262	GGGAGCTAGTGGTTGGGCCCTGGCCCTCTTTTCTATGGTGTCCGCTACAATACCACA	321	
Db	215	GGGAGCTAGTGGTTGGGCCCTGGCCCTCTTTTCTATGGTGTCCGCTACAATACCACA	274	
Qy	322	AACAAATGGCTACCGGGAGTGCCTGGCCAAATGGCAGCTGGGCCCGCCGCTGMAATTACTCC	381	
Db	275	AACAAATGGCTACCGGGAGTGCCTGGCCAAATGGCAGCTGGGCCCGCCGCTGMAATTACTCC	334	
Qy	382	GAGTGCAGAGATCTCTCAATGAGGAGAAAAAGCAAGGTGCACCTACCATGTGCGAGTC	441	
Db	335	GAGTGCAGAGATCTCTCAATGAGGAGAAAAAGCAAGGTGCACCTACCATGTGCGAGTC	394	
Qy	442	ATCATCAACTACTGGGCCACTGTATATCTCCTGGTGGCCCTCTCTGFGGCTTTGTCCTC	501	
Db	395	ATCATCAACTACTGGGCCACTGTATATCTCCTGGTGGCCCTCTCTGFGGCTTTGTCCTC	454	
Qy	502	TTTCTCGGCTCAGGCCAGGCTGCACCAATGGGTGTACCAAGCAGATGAGCCCTGGAG	561	
Db	455	TTTCTCGGCTC-----	466	
Qy	562	GTGGGGCTCCATGGAGTGTGTCGCCCATTTTCAGGTTCGAAGGAGCATCCGGTGCCTGCGA	621	
Db	467	-----AGGAGCATCCGGTGCCTGCGA	487	
Qy	622	AACATCATCACTGGAACTCATCTCGCCTTCATCTCGCAACGCCA	681	
Db	488	AACATCATCACTGGAACTCATCTCGCCTTCATCTCGCAACGCCA	547	
Qy	682	GTCAGTAACCATGAGCCCCGAGGTCCACAGAGCAACGTGGGCTGGTGCAGTGGTG	741	
Db	548	GTCAGTAACCATGAGCCCCGAGGTCCACAGAGCAACGTGGGCTGGTGCAGTGGTG	607	
Qy	742	ACAGCGCCTACAACTACTTCCATGTGACCAACTTCTCTTGGATGTTTCGGCGAGGCTGC	801	
Db	608	ACAGCGCCTACAACTACTTCCATGTGACCAACTTCTCTTGGATGTTTCGGCGAGGCTGC	667	
Qy	802	TACCTGCACACAGCCATCGTGTCTCACCTACTCCACTGACCGGCTGCGCAATGGATGTC	861	
Db	668	TACCTGCACACAGCCATCGTGTCTCACCTACTCCACTGACCGGCTGCGCAATGGATGTC	727	
Qy	862	ATCTGCATTTGGCTGGGGTGGCCCTTCCCAATCATTTGTGGCTGGGCCATTG	913	
Db	728	ATCTGCATTTGGCTGGGGTGGCCCTTCCCAATCATTTGTGGCTGGGCCATTG	779	

RESULT 6
DN396007

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LOCUS       DN396007               581 bp    mRNA    linear    EST 07-MAR-2005
DEFINITION  LIB3935-011-Q6-K6-G12 LIB3935 Canis familiaris cDNA clone
            CLN8913387, mRNA sequence.
ACCESSION   DN396007
VERSION     DN396007.1 GI:60577228
KEYWORDS    EST.
SOURCE      Canis familiaris (dog)
            Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1 (bases 1 to 581)
            Staten,N.R.
            Direct Submission (Staten,N.R.)
            Unpublished (2005)
            Contact: Nick Staten
            Tel: 636 247 6855
            Email: nicholas.r.staten@pfizer.com.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9615"
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                     /clone_lib="LIB3935"
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Query Match	32.6%	Score 515.2	DB 8	Length 581
Best Local Similarity	94.1%	Pred. No. 1.4e-116		
Matches 546	Conservative 0	Mismatches 33	Indels 1	Gaps 1
Qy	734	GGTGTGTGACAGCGGCTACAACTACTTCATCTGACCAACTTCTCTGGATGTCGGCG	793	
Db	3	GGTGTGTGACAGCTGCTACACTCTTCA -GTGACCAACTTCTTCTGGATGTTTGGGG	61	
Qy	794	AGGGCTGTACTGTGCACACAGCCATCGTGTCTACCTACTTCCTGACCGGCTGCGCAAAT	853	
Db	62	AGGGCTGTACTGTGCACACAGGCCATTGTCTTACCTACTTCCACTGACCGGCTGCGCAAAT	121	
Qy	854	GGATGTTTCACTCTGCATTTGGCTTGGGGTGTGCCCTTCCCATCATTTGGCTGGGCCATTG	913	
Db	122	GGATGTTTCACTCTGCATCTGGCTGGGGTGTGCCCTTCCCATCATTTGGCTGGGCCATTG	181	
Qy	914	GGAACTGTACTACGACAAATGAGAAGTGTGTGTTGGCAAAAGCCCTGGGGTGTACACCG	973	
Db	182	GGAACTGTACTACGACAAATGAGAAGTGTGTGTTGGCAAAAGACCTGGGGTGTACACTG	241	
Qy	974	ACTACATCTACCAAGGCCCCATGATCTGGTCTCTGTCTGATCAATTTTCATCTTCTTTTCA	1033	
Db	242	ACTACATCTACCAAGGCCCCATGATCTGGTCTCTGTCTGATCAATTTTCATCTTCTTTTCA	301	
Qy	1034	ACATGTCGCGATCTCTATGACCAAGCTCGGGCATTCACACAGCTGTGAGACATTTCAGT	1093	
Db	302	ACATGTCGCGATCTTATGACCAAACTCGGGCATTCACACATCTGTGAGACATTTCAGT	361	
Qy	1094	ACAGGAAGGCTGTGAAGACCACTCTGGTGTCTGTCGCCCTCTCTGGGCATCACCTACATGC	1153	
Db	362	ACAGGAAGGCTGTGAAGGCCACTCTGGTGTCTGTTTCCCTCTCTGGGCATCACGTACATGC	421	
Qy	1154	TGTTCTTTCGTCAATCCCGGGAGGATGAGGTCTCCGGGGTGTCTTTCATCTACTTCAACT	1213	
Db	422	TGTTCTTTCGTAAACCCCGGGAGGACAGGTCTCTCCCGGGTCACTTTCATCTACTTCAACT	481	
Qy	1214	CTTCTCTGGATCCCTTCCAGGGCTCTTTGTGTCTGTGTCTACTGTCTTCTCAATAGTG	1273	
Db	482	CTTCTCTAGAAATCCCTTCCAGGGTCTTCTTTGTGTGTGTATTTCTACTGTTCCTCAACAGTG	541	
Qy	1274	AGGTCGGTCTCTGCGATCCCGGAAGAGGTGGCACCGGTGGCA	1313	

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Db          542 AGGTCCGCTCTGCCATCCGAAGAGGTGGCATCGATGCA 581
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RESULT 7
DR002290
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

DR002290 727 bp mRNA linear EST 17-MAY-2005
TC110860 Human fetal brain, large insert, pCMV expression library
Homo sapiens cDNA clone TC110860 5' similar to Homo sapiens
corticotropin releasing hormone receptor 1 (CRHR1), mRNA sequence.
DR002290.1 GI:56262163
EST.
Homo sapiens (human)
Homo sapiens
Mammalia; Eutheraia; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheraia; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 727)
Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M.,
Zhang, X., Jay, G. and He, W.
High-throughput cloning of full-length human cDNAs directly from
cDNA libraries optimized for large and rare transcripts
Unpublished (2005)
Contact: Kovacs, KF
High Throughput cDNA Cloning
OriGene Technologies, Inc. ( www.origene.com )
6 Taft Court, Suite 100, Rockville, MD 20850, USA
Tel: 301 340 3188
Fax: 301 340 8606
Email: CDNA@origene.com
This EST submission is part of an on-going human full-length
cloning project at OriGene Technologies, Inc.
Please contact OriGene for access.
OriGene Technologies, Inc.
6 Taft Ct. Suite 100
Rockville, MD 20850
Tel: (301) 340-3188
http://www.origene.com
Seq primer: pCMV6 5prime forward vector primer, OriGene
Technologies Inc.
Location/Qualifiers
1. 727
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TC110860"
/tissue type="Fetal Brain"
/clone lib="Human fetal brain, large insert, pCMV
expression library"
/note="Organ: Fetal Brain; Vector: pCMV6-XL4; Site 1:
EcoRI; Site2: XhoI/SalI compatible end ligatio; Oligo-dT
primed reverse transcription optimized for large and GC
rich mRNA transcripts, cDNA size selection, optimized
ligation for large inserts into mammalian expression
vector, random clones selected for end sequence
verification of full-length genes"

ORIGIN
Query Match 32.5%; Score 514.4; DB 8; Length 727;
Best Local Similarity 99.8%; Pred. No. 2.4e-116;
Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGAGCCCGCAGCCGCCCGCGTTCCTCTGGGATGTCGTAGGACCCGGGCAATTCAGGAC 60
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Qy 61 GGTAGCCGAGCCGAGCCGAGAGTCGGAGGACCCGCGAGCTCCCTCTGCTCAAGGCCCTT 120
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Db 175 GGTAGCCGAGCCGAGCCGAGAGTCGGAGGACCCGCGAGCTCCCTCTGCTCAAGGCCCTT 234
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Qy 121 CTCCTTCTGGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACACCAAGCACTGAGAGCGCTG 180
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SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Pan.
 REFERENCE 1 (bases 1 to 1140)
 AUTHORS Clark, A.G., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1140)
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
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 Best Local Similarity 66.7%; Pred. No. 3.3e-103;
 Matches 756; Conservative 0; Mismatches 278; Indels 99; Gaps 4;
 QY 152 CCCTCCAGGACCACTGCGAGAGCTGCTCCCTGGCCAGCAACATCTAGGAC----- 205
 DB 98 CACTTCTGGAGCAGTACTGCGCACCACTATGACCTTCCACCACTCTCAGGTCCTACT 157
 QY 206 TGCAAGTCAACGATCGTGGACCTCATTTGGCACTGTGCGCCCGCAGCCCTGCGGGG 265
 DB 158 CCTACTGCAACAGACCTTGGACAGATCGAAGTGTGCGCCCGCAGCGCTGCGGGAG 217
 QY 266 AGCTAGTGGTTCGGCCCTGCGCTCTTTTCTATGTGTGTCCTCAATACCAACAA 325
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 QY 326 ATGGTACCGGAGTGGCTGGCCATGGAGCTGGGCGCGCCGGTGAATTAATCTCGAGT 385
 DB 278 ATGCTATCGAAGATGTTGGAGAATGGAGCTGGGCTTCAAAAGATCAACTACTCAAGT 337
 QY 386 GCACGAGGATCTCAATG---AGAGAAAAAGCAAGTGCACCTACCATGTGCGAGTCA 442
 DB 338 GTAGGCCATTTGGATGACAGCAGAGGAGATGATGACCTGCACTACCGGTGCGCCTTG 397
 QY 443 TCATCAACTACCTGGGCCATGTATCTCCCTGGTGGCCCTCTGTTGGCTTTGTCTCT 502
 DB 398 TCGTCAACTACCTGGGCCATGTGCTATCTGTGGCAGCCCTGGTGGCGCTTCTCTGCTT 457
 QY 503 TTCTGGGCTCAGGCCAGGCTGACCCCATTTGGGGTGCACAGGCGATGGAGCCCTGGAGG 562
 DB 458 TCCT----- 461
 QY 563 TGGGGGCTCCATGAGTGGTGCCCATTTTCAGGTTTGAAGGATCCGGTGGCTGGAA 622
 DB 462 -----GGCCCTGGAGAGATCCGGTGTCTGGGA 490
 QY 623 ACATATCCACTGGAACCTCATCTCCGCCCTTCACTCGCGCAACGCGACCTGTTGTGTG 682
 DB 491 ATGTGATTCACTGGAACCTCATCACCACCTTTATCTCTGCGAAATGTATGTGTGTTCTG 550

QY 683 TCCAGCTAACCTAGACCCCGAGGTCCACACAGGCAACCTGGGCTGTGTCAGGTTGGTGA 742
 DB 551 TGAGCT---CGTTGACCATGAGTGCACGAGAGCAATGAGTCTGTGTCGCCGTGCATCA 607
 QY 743 CAGCCGCCCTACAACTACTTCCATGTGACCAACTTCTTCTGTGATGTTGGCGGAGGCTGCT 802
 DB 608 CCACCATCTTCAACTACTTGTGGTGTGACCAACTTCTTCTGTGATGTTGTGGAAGGCTGCT 667
 QY 803 ACCTGCACACAGCCATCGTGTCACTTCCATCTGACCGGCTGCGCAAAATGATGTTCA 862
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 QY 1043 GCATCTCATGACCAAGCTCGGGGATCCACCACTCTGAGACCATTCAGTACAGGAAG 1102
 DB 908 GGATCTTAATGACAAAGTTACGCGGTGCCACATCCGAGACAAATCCAGTACAGGAAG 967
 QY 1103 CTGTGAAAGCACTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1162
 DB 968 CAGTGAAGGCCACCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1027
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 DEFINITION 3GAL 30M12 5', mRNA sequence.
 ACCESSION CV039433
 VERSION CV039433.1 GI:53558872
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 583)
 AUTHORS Ewok-Clover, C.M., Ashwell, C.M., McMurtry, J.P., Lillehoj, H.S.,
 Matukumalli, L.K. and Van Tassel, C.P.
 TITLE Characterization of expressed sequence tags generated from multiple
 chicken tissues
 JOURNAL Unpublished (2004)
 COMMENT Contact: Christina M. Clover
 Growth Biology Laboratory
 Animal and Natural Resources Institute
 Bldg. 200 Rm215 BARC-East, Beltsville, MD 20705, USA
 Tel: 3015048224
 Fax: 3015048623
 Email: chrisclover@ars.usda.gov
 Single pass sequencing. Bases called and trimmed with phred
 0.000925 using options -trim_alt '-trim_fastaVector identified by
 cross_match using options -mismatch 12 -minscore 12
 Plate: 30 row: M column: 12
 Seq primer: CCGAGTCAAGGCTGTGTAAGAG

High quality sequence stop: 583.
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/clone_lib="BARC 3GAL chicken mixed tissue"
/note="Vector: pBluescript, SK+, Stratagene; Site 1: NotI;
Site 2: EcoRI; Normalized library of pooled RNA isolated
from whole brain, ultimobranchial gland, parathyroid
gland, cecal tonsil and primordial germ cells Multiple"

ORIGIN
Query Match 29.0%; Score 458.2; DB 7; Length 583;
Best Local Similarity 86.6%; Pred. No. 2e-102;
Matches 505; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
QY 647 CCGCCTTCATCTCGGCAAGCCACCTGGTTCGTGTCAGCTAACATGAGCCCGAGG 706
Db 1 CAGCCTTCATCTACGCAATGCCACGTGTTGTGGTGCAGCTCACGATGAACCCAGAG 60
QY 707 TCACACAGACACCTGGGCTGTGTCAGGTGTCAGCGCGCTCAACTACTTCCATG 766
Db 61 CCCACGAGACACGTCGTGTCGCGCTGTCATCTGCTGCTCAATTAATCTTCCATG 120
QY 767 TGACCAACTCTCTTCGTGATGCTCGGCGAGGCTGTACCTGACACAGCCATCGTGCTCA 826
Db 121 TCACCAACTCTCTTCGTGATGCTCGGCGAGGCTGTACCTGACACAGCCATCGTGCTCA 180
QY 827 CCTACTCCACTGACCGGCTGCGCAATGGATGTTCACTGTCATTTGGCTGGGGTGTGCCCT 886
Db 181 CCTATTCCACCGACAAGCTCCGCAAGTGGATGTTCACTGTCATTTGGCTGGTATCCCT 240
QY 887 TCCCATCATTTGGCTGGGCAATGGGAAGCTGTACTAGCAATGAGAAGTGTGCT 946
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Db 301 TTGGGAAGCGAGAGATTTATCTGACTACATCTATCAAGTCCCATGATCTGTGTC 360
QY 1007 TGCTGATCAATTTTCATCTCTTTTCAACATCGTCGCACTCTCATGACCAAGCTCGGG 1066
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DEFINITION Mus musculus CHR2 gene, VIRTUAL TRANSCRIPT, partial sequence, GSS 15-DEC-2003
ACCESSION AY406517
VERSION AY406517.1 GI:39762491
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 1170)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
REFERENCE 2 (bases 1 to 1170)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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source 1. 1170
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/locus_tag="HCM2583"
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Query Match 28.2%; Score 446; DB 10; Length 1170;
Best Local Similarity 67.5%; Pred. No. 2.4e-99;
Matches 722; Conservative 0; Mismatches 255; Indels 93; Gaps 3;
QY 209 AGTGCAACGATCCGTGGACCTCATTTGGCACTGTGGCCCGCCGAGCCCTGCGGGGAGC 268
Db 191 ACTGCAACGACGCTTGGACCATCGGACCTGCTGGCCACAGAGGGCACCCGGAGCCC 250
QY 269 TAGTGTTCGGCCCTGCCCTGCTTTTCTATGGTGTCCGCTACAATACACAAACAATG 328
Db 251 TAGTAGAGAGACGCTGCCCGAGTACTTCAATGGCATCAAGTACAAACACACCGGAATG 310
QY 329 GCTACCGGAGTCCCTGGCCAAATGGCAGCTGGGCGCCCGCCGCTGAATTACTCCGAGTGC 388
Db 311 CCTACAGAGAGTCCCTGGGAAACGGGACCTGGGCCCTCAAGGGTCAACTACTACACTGCG 370
QY 389 AGGAGATCTCTAATG--AGGAGAAAAAAGCAAGGTGCATACCATGTGCGAGTCACTCA 445
Db 371 AACCCTTTTGGATGACAGCAGAGAGATGATGACCTGCAATACCGAATGCCCTCATTTG 430
QY 446 TCAACTACCTGGGCCACTGTATCTCCCTGGTGGCCCTCTCTGGTGGCTTTGTCTCTTTTC 505
Db 431 TCAACTACCTGGGCTACTGTGTTTCCGTGGTGGCCCTTGGTGGCCGCTTTCTCTGCTTTTC 490
QY 506 TGGCGCTCAGGCCAGCTGCACCCATGGGGTGACACGAGCATGGAGCCCTGGAGGTGG 565
Db 491 T-----AGTGTGGGAGTATCCGCTGCTGAGGATG 491
QY 566 GGGCTCCATGGAGTGGTGGCCCATTTTCAGGTTTCGAAGGAGCATCCGGTGGCTGGGAACA 625
Db 492 -----AGTGTGGGAGTATCCGCTGCTGAGGATG 523
QY 626 TCATCCACTGGAACTCATCTCGCCCTTCATCTCGGCAACGCCACCTGGTGTGGTGTGC 685
Db 524 TGATCCACTGGAACTCATCACCACTTCATCTGAGAAACATCCGCTGGTGTCTCTGTGTC 583
QY 686 AGCTAACCATGAGCCCGAGGTCCACAGAGCAACGTGGGCTGGTGGAGTGTGGTGCAG 745
Db 584 AACT---CATCGACCAAGTGCAGAGGCAATGAGGTCTGGTGGCTGCACTCACCA 640
QY 746 CCGCCTACACTACTTCCATGTGACCAACTTCTTCTGGATGTTCTGGGAGGGCTGTCTACC 805
Db 641 CCATCTTCAACTATTTTGTGGTCAACCAACTTCTTCTGGATGTTTGTGGAGGGCTGTCTACC 700

Search completed: March 17, 2006, 14:35:37
Job time : 5893 secs

Location/Qualifiers
1. .766

ORIGIN

Query Match	27.7%;	Score 438.2;	DB 8;	Length 766;
Best Local Similarity	79.1%;	Pred. No. 1.9e-97;		
Matches 521;	Conservative 0;	Mismatches 138;	Indels 0;	Gaps 0;
QY	787	TTCGGGAGGGCTGCTACCTG	CACAGCCATCGTGTCTCACTT	CCTACTCCACTGACCGGCTG 846
DB	1	TTTGGGGAGGGCTGTTACCT	TACACAGCGCTATTGTGCTAA	CTACTCGACCGCAAACTG 60
QY	847	CGCAATGGATGTCATCTGC	ATTGGCTGGGCTGCCCTTCCC	CCATCTGTGGCCTGG 906
DB	61	CGCAATGGATGTCATCTGT	ATCGGCTGGTATTCCCTTCCC	ATCATTTGTGGCTTGG 120
QY	907	GCCATTGGGAAGCTGTACT	ACGCAATGAGAAGTGCTGTT	GTGCAAAAGCCTGGGGTG 966
DB	121	GCCATTGGCAAACTTTACT	ATATGCAATGAAAAGTGCTGG	TTTGTTAGAAGCAGGAGTC 180
QY	967	TACACCGCATACATCTACC	AGGGCCCCCATGATCTCGT	CTCGTGTGATCAATTTTCATCTTC 1026
DB	181	TACACAGATTTTATCTACC	AGGAGACGGTTATCCTTGT	ACTGTCTGTCATCACTTTATATT 240
QY	1027	CTTTTCAACATCGTCGG	CACTCTCATGACCAAGCTCG	GGGCATCCACCAAGTCTGAGACC 1086
DB	241	TTATTCAACATAGTGC	GGATTCTGATGACAAAAG	CTCGAGCTTCCACCACTTCAGAGACC 300
QY	1087	ATTTCAGTACAGGAAG	CGTGTGAAGGCACTCTCT	GGTGTGCTGTGCCCTCTCTGGGCAATCACC 1146

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